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STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Wednesday, April 05, 2006 11:25 AM
To: STIC-Biotech/ChemLib
Subject: Re:10/067832

Importance: High

Please search SEQ ID NO: 2 and protein encoded by SEQ ID NO 1 and 13.

Thanks.

J.Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM nucleic - protein search, using **frameplus.n2p model**
Run on: April 7, 2006, 23:31:58 ; Search time 31.8263 Seconds
(without alignments)
1021.610 Million cell updates/sec

Title: US-10-067-832D-1
Perfect score: 665
Sequence: 1 gtccaggagattacagctc.....tttgatgctgcaaaaaaaa 370

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWEB spool/US10067832/runat_07042006_175609_9682/app_query.fasta.1
-DB=A Geneseq -QMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes02p
-USER=US10067832 @CGN 1.1 476 @runat_07042006_175609_9682 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	418	62.9	89	4 AAM41466	Aam41466 Human pol
2	418	62.9	115	5 ABP41331	Abp41331 Human ova
3	394	59.2	73	2 AAY08413	Aay08413 P. Obesius
4	394	59.2	73	3 AAB36290	Aab36290 Isracali s
5	394	59.2	73	4 AAM39680	Aam39680 Human pol
6	339	51.0	73	4 AAB59910	Abbs59910 Drosophila
7	313	47.1	73	3 AAG41925	Aag41925 Arabidops
8	313	47.1	96	3 AAG41924	Aag41924 Arabidops
9	312	46.9	73	3 AAG40885	Aag40885 Zea mays

10	300	45.1	73	3 AAG27281	Aag27281 Zea mays
11	285	42.9	73	8 ADT58384	Adt58384 Plant pol
12	252	37.9	89	5 ADH32312	Adh32312 Novel Yea
13	252	37.9	320	6 ABR83620	AbR83620 HUB1-GFP
14	163	24.5	33	2 AAY08414	Aay08414 Human bea
15	163	24.5	33	8 ADR43346	Adr43346 Human bea
16	160.5	24.1	112	8 ADX97089	Adx97089 Plant ful
17	160.5	24.1	112	8 ADX78384	Adx78384 Plant ful
18	158	23.8	112	8 ADY06931	Ady06931 Plant ful
19	158	23.8	113	8 ADY05953	Ady05953 Plant ful
20	158	23.8	128	8 ADX96955	Adx96955 Plant ful
21	147.5	22.2	32	3 AAB36291	Aab36291 Human bea
22	138	20.8	27	4 AAM21187	Aam21187 Peptide #
23	138	20.8	27	4 ABB43508	Abb43508 Peptide #
24	138	20.8	27	4 AAM37402	Aam37402 Peptide #
25	138	20.8	27	4 ABB26468	Abb26468 Protein #
26	138	20.8	27	4 AAM77251	Aam77251 Human bon
27	138	20.8	27	4 AAM64443	Aam64443 Human bra
28	138	20.8	27	5 ABG46267	Abg46267 Human pep
29	138	20.8	110	8 ADY04784	Ady04784 Plant ful
30	137	20.6	40	8 ADY04557	Ady04557 Plant ful
31	137	20.6	40	8 ADY95411	Ady95411 Yeast ubi
32	137	20.6	104	5 ADH32742	Adh32742 Yeast smo
33	133	20.0	40	9 ADY95410	Ady95410 Yeast ubi
34	120	18.0	32	9 ADV95409	Adv95409 Yeast ubi
35	115	17.3	32	9 ADX39713	Adx39713 HIV Env p
36	88.5	13.3	854	9 ADX39709	Adx39709 HIV Env p
37	85.5	12.9	857	9 ADX39712	Adx39712 HIV Env p
38	85	12.8	857	9 ADX39712	Adx39712 HIV Env p
39	83.5	12.6	638	9 ADZ07768	Adz07768 HIV CON-A
40	83.5	12.6	854	9 ADZ07767	Adz07767 HIV CON-A
41	83.5	12.6	854	9 ADZ07767	Adz07767 HIV CON-A
42	82.5	12.4	853	9 ADZ04172	Adz04172 HIV prote
43	82	12.3	831	9 ADZ07806	Adz07806 HIV CON-F
44	80	12.0	123	8 ADY05551	Ady05551 Plant ful
45	80	12.0	125	8 ADY05562	Ady05562 Plant ful

ALIGNMENTS

RESULT 1
AAM41466
ID AAM41466 standard; protein; 89 AA.
XX AAM41466;
AC AAM41466;
XX AC
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6397.
XX Human polypeptide SEQ ID NO 6397.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US034263.
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-0052317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Dmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI60622.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 6397; 10078pp; English.
 XX
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 89 AA;
 Alignment Scores:
 Pred. No.: 1,03e-41 Length: 89
 Score: 418.00 Matches: 78
 Percent Similarity: 96.3% Conservative: 1
 Best Local Similarity: 95.1% Mismatches: 3
 Query Match: 62.9% Indels: 0
 DB: Gaps: 0
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 QY 2 TTCACGAGATTACACTCCAGCCACATGATTGAGTGGTGTTCACACGCTTAGCA 61
 DB 8 PheGluAlaIleArgAlaProAlaArgMetIleGluValValCysAenAspArgLeuGly 27
 QY 62 AGAAGTCCGCTTAAGTGCACACCGATGACCCATCGGGACTTGAAGAACTGATA 121
 DB 28 LysLysValArgValLysCysAenThrAspAspThrIleGlyAspLeuLysLeuIle 47
 QY 122 GCGGCCCAACTGGCACTCGTTGGAATAGATCGTTCTTAAAGTGGTACACGATTTT 181
 DB 48 AlaAlaGlnThrGlyThrArgTrpAsnLysIleValLeuLysIleTrpThrIlePhe 67
 QY 182 AAGGACCATGTATCTCTGGAGATTATGAATCCACATGGGATGACCTGGAGCTTTAT 241
 DB 68 LysAspHisValSerLeuGlyAspTyrGluIleHisAspGlyMetAsnLeuGluLeuTyr 87
 QY 242 TACCAG 247
 DB 88 TyrGln 89
 RESULT 2
 ABP41331
 ID ABP41331 standard; protein; 115 AA.
 AC ABP41331;
 XX
 XX 22-AUG-2002 (first entry)
 DT Human ovarian antigen HACNC39, SEQ ID NO:2463.
 XX
 DE

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX Homo sapiens.
 XX WO200200677-A1.
 XX 03-JAN-2002.
 XX 07-JUN-2001; 2001WO-US018569.
 XX 07-JUN-2000; 2000US-0209467P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 XX N-PSDB; ABQ54408.
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 XX cancer), immune disorders, cardiovascular disorders and neurological
 XX diseases.
 XX Claim 11; SEQ ID NO 2463; 2922pp; English.
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 XX encompasses polypeptides 90% identical and polynucleotides 95% identical
 XX to the sequences of the invention. The invention additionally relates to
 XX recombinant vectors and host cells comprising human ovarian antigen
 XX polynucleotides, antibodies against human ovarian antigens, and the use
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
 XX treating, prognosing or preventing various ovary and/or breast-related
 XX disorders. Such conditions include ovarian cancer and breast cancer, and
 XX metastatic tumours of ovarian or breast origin, reproductive system
 XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
 XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 XX vaginitis), immune disorders (e.g., congenital and acquired
 XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
 XX respiratory disorders, neurological disorders, gastrointestinal disorders
 XX and urinary system disorders. Ovarian antigen polypeptides and
 XX polynucleotides may also be used in screening for compounds which
 XX modulate ovarian antigen expression or activity. The polynucleotides may
 XX further be used for gene therapy, chromosome mapping, in the
 XX identification of individuals and in forensic analysis, and the
 XX polypeptides may be used as food additives or to prepare antibodies
 XX useful in disease diagnosis, drug targeting and phenotyping. The present
 XX sequence represents a human ovarian antigen of the invention. Note: The
 XX sequence data for this patent did not form part of the printed from WIPO
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 115 AA;
 Alignment Scores:
 Pred. No.: 1.1e-41 Length: 115
 Score: 418.00 Matches: 78
 Percent Similarity: 96.3% Conservative: 1
 Best Local Similarity: 95.1% Mismatches: 3

CC useful in diagnosis of conditions as above

XX SQ Sequence 73 AA;

Alignment Scores:

Pred. No.: 8,25e-39 Length: 73

Score: 394.00 Matches: 73

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 59.2% Indels: 0

DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x AAY08413 (1-73)

QY 29 ATGATTGAGTGGTGGTTCGACACGACCTCTAGGAGAAAGTTCGGTTCGACACACACC 88

DB 1 MetileGluValValCysAsnAspArgLeuGlyLysValValArgValLysCysAsnThr 20

QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAAT 148

DB 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40

QY 149 AAGATCGTTCTTAAAGTGGTACAGATTTTAAAGACCATGTATCTCTGGAGATTAT 208

DB 41 LysIleValLeuLysLysTrpThrIlePheLysAspHisValSerLeuGlyAspTyr 60

QY 209 GAAATCCAGTGGGATGAACCTGGAGCTTTATTACCAG 247

DB 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTrpGln 73

RESULT 4

AAB36290

ID AAB36290 standard; protein; 73 AA.

XX AC AAB36290;

XX DT 23-FEB-2001 (first entry)

XX DE Israeli sand rat beacon ligand.

XX KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes; ligand.

XX OS Psammomys obesus.

XX PN WO200064931-A1.

XX PD 02-NOV-2000.

XX PF 19-APR-2000; 2000WO-AU000342.

XX PR 23-APR-1999; 99AU-00009919.

XX PR 24-MAR-2000; 2000AU-00006454.

XX PA (AUTO-) AUTOGEN PTY LTD.

XX PI Collier G, Walder K, Zimmet P;

XX DR WPI; 2000-687311/67.

XX DR N-PSDB; AAC81767.

XX PT Ligand of beacon protein useful for treating obesity, anorexia, energy imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and insulin resistance.

XX PS Claim 3; Fig 1; 67pp; English.

XX CC The present invention is related to the isolation of a ligand known as beacon from the Israeli sand rat. Beacon is associated with the regulation of energy balance, and the protein, its coding sequence and analogues can be used in the treatment of diabetes, obesity, anorexia, energy imbalance, metabolic syndrome, dyslipidemia, hypertension and insulin resistance. In addition, they can be used in agriculture to

Query Match: 62.9% Indels: 0

DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x ABP41331 (1-115)

QY 2 TTCACGAGGATTACAGCTCCAGCCACATGATTGAGTGGTTCGACACGCTCTAGGA 61

DB 34 PheGluAlaIleArgAlaProAlaArgMetIleGluValValCysAsnAspArgLeuGly 53

QY 62 AAGAAAGTCGCGCTTAAGTGCACACCGATGACACCATCGGGGACTTGAAGAACTGATA 121

DB 54 LysLysValArgValLysCysAsnThrAspAspThrIleGlyAspLeuLysLeuIle 73

QY 122 GCGGCCCAACTGGCACTCTGTTGGAATAAGATCGTTCTTAAAGTGGTACAGATTTT 181

DB 74 AlaAlaGlnThrGlyThrArgTrpAsnLysIleValLeuLysLysTrpThrIlePhe 93

QY 182 AAGGACCATGTATCTCTGGGAGATTATGAATCCAGATGGGATGACCTGGAGCTTTAT 241

DB 94 LysAspHisValSerLeuGlyAspTyrGluIleHisAspGlyMetAsnLeuGluLeuTyr 113

QY 242 TACCAG 247

DB 114 TyrGln 115

RESULT 3

AAY08413

ID AAY08413 standard; protein; 73 AA.

XX AC AAY08413;

XX DT 24-JUL-1999 (first entry)

XX DE P. obesus beacon protein.

XX KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment; obesity; anorexia; weight maintenance; energy imbalance; diabetes; metabolic syndrome; dyslipidemia; hypertension; insulin resistance; medicament; livestock; diagnosis.

XX OS Psammomys obesus.

XX PN WO9923217-A1.

XX PD 14-MAY-1999.

XX PF 30-OCT-1998; 98WO-AU000902.

XX PR 31-OCT-1997; 97AU-00000117.

XX PR 11-NOV-1997; 97AU-00000323.

XX PA (ITDI-) INT DIABETES INST.

XX PA (UYDE-) UNIV DEAKIN.

XX PI Zimmet PZ, Collier G;

XX DR WPI; 1999-337484/28.

XX DR N-PSDB; AAX57359.

XX PT New gene encoding a beacon protein associated with modulation of obesity, diabetes and metabolic energy levels.

XX PS Claim 2; Page 50; 85pp; English.

XX CC This invention describes a novel beacon protein and its encoding nucleic acid which is expressed in larger amounts in hypothalamus tissue of obese animals compared to lean animals. Agonists and antagonists of beacon can be used to treat obesity, anorexia, weight maintenance, energy imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin resistance. The beacon protein, itself is used to manufacture medicaments for treatment of obesity, anorexia, energy imbalance or diabetes. The treatment is contemplated for both human and animals, such as those important to the livestock industry. The antibody and polynucleotides are

Query Match: 62.9% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x ABP41331 (1-115)

QY 2 TTCACGAGGATTACAGCTCCAGCCACCAATGATGAGTGGTTGGACGACCGTTCAGGA 61
DB 34 PhGluAlaIleArgAlaProAlaArgMetIleGluValValCysAsnAspArgLeuGly 53
QY 62 AAGAAAGTCGCGCTTAAGTGCACACCGATGACACCATCGCGGACTTGAAGAACTGATA 121
DB 54 LysLysValArgValLysCysAsnThrAspAspThrIleGlyAspLeuLysLeuIle 73
QY 122 GCGGCCCAACTGCGCTCTGCTGGCAATAGATGCTTCTTAAAGTGGTACAGATTTT 181
DB 74 AlaAlaGlnThrGlyThrArgTrpAsnLysIleValLeuLysLysTrpTrpThrIlePhe 93
QY 182 AAGGACCATGTATCTCTGGGAGATTATGAATCCACGATGGGATGACCTGGAGCTTTAT 241
DB 94 LysAspHisValSerLeuGlyAspTrpGluIleHisAspGlyMetAsnLeuGluLeuTyr 113
QY 242 TACCAG 247
DB 114 TyrGln 115

RESULT 3
AAY08413
ID AAY08413 standard; protein; 73 AA.
XX AC AAY08413;
XX DT 24-JUL-1999 (first entry)
XX DE P. obesus beacon protein.
XX KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment; obesity; anorexia; weight maintenance; energy imbalance; diabetes; metabolic syndrome; dyslipidemia; hypertension; insulin resistance; medicament; livestock; diagnosis.
XX OS Peannomya obesus.
XX PN WO9923217-AL.
XX PD 14-MAY-1999.
XX PF 30-OCT-1998; 98WO-AU000902.
XX PR 31-OCT-1997; 97AU-00000117.
XX PT 11-NOV-1997; 97AU-00000323.
XX (ITDI-) INT DIABETES INST.
XX PA (UYDE-) UNIV DEAKIN.
XX PI Zimmet PZ, Collier G;
XX PI 1999-337484/28.
XX DR N-PSDB; AAX57359.
XX PT New gene encoding a beacon protein associated with modulation of obesity, diabetes and metabolic energy levels.
XX PS Claim 2; Page 50; 85pp; English.
XX This invention describes a novel beacon protein and its encoding nucleic acid which is expressed in larger amounts in hypothalamus tissue of obese animals compared to lean animals. Agonists and antagonists of beacon can be used to treat obesity, anorexia, weight maintenance, energy imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin resistance. The beacon protein, itself is used to manufacture medicaments for treatment of obesity, anorexia, energy imbalance or diabetes. The treatment is contemplated for both human and animals, such as those important to the livestock industry. The antibody and polynucleotides are

CC useful in diagnosis of conditions as above
XX SQ Sequence 73 AA;
Alignment Scores:
Pred. No.: 8,25e-39 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x AAY08413 (1-73)

QY 29 ATGATTGAGTGGTTTTCACACGACCGCTTAGGAAAGAAAGTCCGGTTAAGTGCACACC 88
DB 1 MetIleGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 20
QY 89 GATGACACCATCGCGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAA 148
DB 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40
QY 149 AAGATCGTTCTTAAAGTGGTACAGATTTTAAAGGACCATGTATCTCTGGAGATTAT 208
DB 41 LysIleValLeuLysLysTrpTrpThrIlePheLysAspHisValSerLeuGlyAspTyr 60
QY 209 GAAATCCACGATGGGATGAACCTGGAGCTTTATTACCAG 247
DB 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTrpGln 73

RESULT 4
AAB36290
ID AAB36290 standard; protein; 73 AA.
XX AC AAB36290;
XX DT 23-FEB-2001 (first entry)
XX DE Israeli sand rat beacon ligand.
XX KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes; ligand.
XX OS Peannomya obesus.
XX PN WO200064931-AL.
XX PD 02-NOV-2000.
XX PF 19-APR-2000; 2000WO-AU000342.
XX PR 23-APR-1999; 99AU-00009919.
XX PT 24-MAR-2000; 2000AU-00006454.
XX (AUTO-) AUTOGEN PTY LTD.
XX PI Collier G, Walder K, Zimmet P;
XX PI 2000-687311/67.
XX DR N-PSDB; AAC81767.
XX PT Ligand of beacon protein useful for treating obesity, anorexia, energy imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and insulin resistance.
XX PS Claim 3; Fig 1; 67pp; English.
XX The present invention is related to the isolation of a ligand known as beacon from the Israeli sand rat. Beacon is associated with the regulation of energy balance, and the protein, its coding sequence and analogues can be used in the treatment of diabetes, obesity, anorexia, energy imbalance, metabolic syndrome, dyslipidemia, hypertension and insulin resistance. In addition, they can be used in agriculture to

```

CC produce leaner animals
XX
SQ Sequence 73 AA;

Alignment Scores:
Pred. No.:      8.25e-39      Length:      73
Score:          394.00      Matches:      73
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      59.2%      Indels:      0
DB:              3          Gaps:      0

US-10-067-832D-1 (1-370) x AAM36290 (1-73)
QY 29 ATGATTGAGTGGTTTGCACACCGCTTAGGAAAGAAAGTCCGCTTAAGTGCACACC 88
   |||||
Db 1 MetIleGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGGCACTCGTTGGAT 148
   |||||
Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40
QY 149 AAGATCCACGATGGGATGAACCTGGAGCTTTATTACCAG 247
   |||||
Db 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrGln 73

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AAM39680
ID AAM39680 standard; protein; 73 AA.
AC AAM39680;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2825.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSB-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AAI58836.

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XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2825; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX SQ Sequence 73 AA;

Alignment Scores:
Pred. No.:      8.25e-39      Length:      73
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RESULT 6
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ID ABB59910 standard; protein; 73 AA.
XX
XX ABB59910;
XX
XX 26-MAR-2002 (first entry)
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XX Drosophila melanogaster polypeptide SEQ ID NO 6522.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.

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XX PA. (PEKE) PE CORP NY.
XX FI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL04013.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX PS Disclosure; SEQ ID NO 6522; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB160511), expressed DNA
XX sequences (AB161840-AB16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
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XX Pred. No.: 4.2e-32 Length: 73
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XX Best Local Similarity: 86.3% Mismatches: 7
XX Query Match: 51.0% Indels: 0
XX DB: 4 Gaps: 0
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XX DT 18-OCT-2000 (first entry)
XX XX
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52222.
XX XX
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX XX
XX OS Arabidopsis thaliana.
XX XX
XX PN EP1033405-A2.
XX XX
XX PD 06-SEP-2000.
XX XX

PF 25-FEB-2000; 2000EP-00301439.
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RESULT 8

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XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 52221.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN BP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-00301439.

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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 6,7e-29
Score: 313.00
Percent Similarity: 88.9%
Best Local Similarity: 80.6%
Query Match: 47.1%
DB: 3

US-10-067-832D-1 (1-370) x AAG41924 (1-96)

QY 29 ATGATTGAGTGGTTTCAACGACCGCTAGGAAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 24 MetileuValValLeuAenAspArgLeuGlyValArgValArgValLysCysAsnAsp 43
QY 89 GATGACACCATCGGGACTTGAAGAACTGATAGCGGCCCAAACTGCACCTCGTTGGAAT 148
Db 44 AspAspThrileGlyAspLeuLysLeuValAlaAlaGlnThrGlyThrArgAlaGlu 63
QY 149 AAGATCCTTCTTAAAGTGGTACACCATTTTAAAGCACCATGTATCTCTCGGAGATTAT 208
Db 64 LysileArgileGlnLysTrpTyAsnileTyriLysAspHisileThrLeuLysAspTy 83
QY 209 GAAATCACCATGGGAGAACCTCGAGCTTTATTAC 244
Db 84 GlulleHisaspGlyMetGlyLeuGlulLeuTyTy 95

RESULT 9
AAG40885
ID AAG40885 standard; protein; 73 AA.
XX
AC AAG40885;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 50790.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 01-APR-1999; 99US-0127462P.
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PR 19-APR-1999; 99US-0130077P.
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PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR	21-JUL-1999;	99US-0145087P.
PR	22-JUL-1999;	99US-0145085P.
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PR	22-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
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PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151085P.
PR	27-AUG-1999;	99US-0151086P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151913P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
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PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155113P.
PR	23-SEP-1999;	99US-0155486P.
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PR	28-SEP-1999;	99US-0156458P.
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PR	08-OCT-1999;	99US-0158232P.
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PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
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PR	18-OCT-1999;	99US-0159638P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	22-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
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PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Alignment Scores:		
Pred. No.:	8,248-29	Length: 73
Score:	312.00	Matches: 58
Percent Similarity:	88.9%	Conservative: 6
Best Local Similarity:	80.6%	Mismatches: 8
Query Match:	46.9%	Indels: 0
DB:	3	Gaps: 0
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Db	1	MetileGluValValLeuAenAspArgLeuGlyLysLysValArgValLysCysAenGlu 20
Qy	89	GATGACACCATCGGGGACTTGAAGAACTAGTAGCGGCCCAAACTGGCCTCGTTGGAAT 148

Db 21 AspAspThrIleGlyAspLeuLysLeuValalaGlnThrGlyThrArgProGlu 40
QY 149 AAGATCGTTCTTTAAAGTGGTACACGATTTTAAAGACCATGATCTCTGGGAGATTAT 208
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 41 LysileArgileGlnIlystrpTyraenilleTyrlsAsphisleThrLeuLysAspTy 60
QY 209 GAAATCCAGCATGGATGAACCTGGAGCTTTATTAC 244
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Db 61 GluileHisaspGlyMetGlyLeuGluLeuTyrr 72

RESULT 10
AAG27281
ID AAG27281 standard; protein; 73 AA.
AC AAG27281,
XX
XX
DT 17-OCT-2000 (first entry)
XX
XX Zea mays protein fragment SEQ ID NO: 32055.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
XX Zea mays subsp. mays.
XX
XX
PN EP1033405-A2.
XX
PD
PD
XX 06-SRP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 20-JUL-1999; 99US-0144352P.
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PR 06-AUG-1999; 99US-0147416P.
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PR 10-AUG-1999;	99US-0148171P.	DB:	3	Gaps:	0
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PR 17-AUG-1999;	99US-0149175P.				
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PR 23-AUG-1999;	99US-0149930P.				
PR 25-AUG-1999;	99US-0150586P.	QY 209 GAAATCCAGATGGATGAACTGACCTGGAGCTTTATTAC 244			
PR 26-AUG-1999;	99US-0150884P.	Db 61 GluValHisAspGlyMetGlyLeuGluLeuTyrTyr 72			
PR 27-AUG-1999;	99US-0151066P.				
PR 27-AUG-1999;	99US-0151080P.				
PR 30-AUG-1999;	99US-0151303P.				
PR 31-AUG-1999;	99US-0151438P.				
PR 01-SEP-1999;	99US-0151930P.	RESULT 11			
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PR 15-SEP-1999;	99US-0154018P.	AC ADTS8384;			
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PR 20-SEP-1999;	99US-0154779P.	DT 13-JAN-2005 (first entry)			
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PR 23-SEP-1999;	99US-0155486P.	DE Plant polypeptide, SEQ ID 8461.			
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PR 28-SEP-1999;	99US-0156536P.	KW disease resistance; galactomannan production; plant growth regulator;			
PR 04-OCT-1999;	99US-0157117P.	KW heat tolerance; herbicide tolerance; lignin production;			
PR 05-OCT-1999;	99US-0157753P.	KW extreme osmotic condition tolerance; pathogens resistance;			
PR 06-OCT-1999;	99US-0157865P.	KW pest resistance; yield improvement; seed oil yield; seed protein yield.			
PR 07-OCT-1999;	99US-0158029P.	XX			
PR 08-OCT-1999;	99US-0158232P.	OS Viridiplantae.			
PR 12-OCT-1999;	99US-0158369P.	XX			
PR 13-OCT-1999;	99US-0159293P.	PN US2004216190-A1.			
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PR 14-OCT-1999;	99US-0159329P.	XX			
PR 14-OCT-1999;	99US-0159330P.	PF 18-DEC-2003; 2003US-00739930.			
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PR 21-OCT-1999;	99US-0160814P.	XX			
PR 21-OCT-1999;	99US-0160815P.	DR WPI; 2004-757369/74.			
PR 22-OCT-1999;	99US-0160980P.	XX			
PR 22-OCT-1999;	99US-0160981P.	PT New recombinant DNA constructs useful in the field of biochemistry and			
PR 22-OCT-1999;	99US-0160989P.	PT Genetics, and in particular for producing transgenic plants with improved			
PR 22-OCT-1999;	99US-0161404P.	XX biological characteristics.			
PR 25-OCT-1999;	99US-0161405P.	PS Claim 2; SEQ ID NO 8461; 14pp; English.			
PR 25-OCT-1999;	99US-0161406P.	XX			
PR 26-OCT-1999;	99US-0161359P.	CC The invention relates a recombinant DNA construct comprising a			
PR 26-OCT-1999;	99US-0161360P.	CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:			
PR 26-OCT-1999;	99US-0161361P.	CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences			
PR 28-OCT-1999;	99US-0161920P.	CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,			
PR 28-OCT-1999;	99US-0161992P.	CC Arabidopsis, wheat and rape but the specification does not indicate which			
PR 28-OCT-1999;	99US-0161993P.	CC sequences is derived from which organism. Also included is a method of			
PR 28-OCT-1999;	99US-0162142P.	CC producing a plant having an improved property, comprising transforming a			
		CC plant with a recombinant DNA construct comprising a promoter region			
		CC functional in a plant cell operably joined to a polynucleotide encoding a			
		CC polypeptide associated with the property, and growing the transformed			
		CC plant. The property is selected from improving plant cold tolerance, for			
		CC manipulating growth rate in plant cells by modification of the cell cycle			
		CC pathway, for improving plant drought tolerance, for providing increased			
		CC resistance to plant disease, for galactomannan production, for production			

Alignment Scores:		
Pred. No.:	2.4e-27	73
Score:	300.00	55
Percent Similarity:	87.5%	8
Best Local Similarity:	76.4%	9
Query Match:	45.1%	0
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		

of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

US-10-067-832D-1 (1-370) x ADT58384 (1-73)

29	ATGATTGAGCGTGGTTGGCAACAGCAGCGTCTAGAGAAAGAAAGTCCTGCGGTAACTGATCGAACACC	88
Qy		
Db		
1	MetIleGluValValLeuAsnAspArgLeuGlyLysLysValArgValLysCys----	19
Qy		
Db		
89	GATGACACCATCGGGACCTTGAAGAAACTGATAGCGGCCCAACTGGC--ACTCGTTGG	149
Qy		
Db		
20	AspAspThrIleGlyAspLeuLysLysLeuValAlaIleGlnThrGly***ThrArgPro	39
Qy		
Db		
146	AATAAGCATCGTTTAAAAAGTGTACACGATTTTAAAGACCACCATGTATCTCTGGGAGAT	205
Qy		
Db		
40	GluLysIleArgIleGlnLysTrpTrpAsnIleTyrLysAspHisIleThrLeuLysAsp	59
Qy		
Db		
206	TATGAATCCAGATGGGATGAACCTGGAGCTTTATTAC	244
Qy		
Db		
60	TyrGluValHisAspGlyMetGlyLeuGluLeuTyrTyr	72
Qy		
Db		

RESULT 12

ADH32312
ID ADH32312 standard; protein: 89 AA.

AC ADH32312:

11-MAR-2004 (Friday)

DE Nove] veast smORP572-encoded no]vmentide. SEO ID NO.770
XX

Open reading frame; ORF, identification; in silico; yeast; smORF;
KW small open reading frame; antisense therapy; antibody therapy;
KW drug screening; fungal infection; fungicide; gene therapy; vaccine.
KW

OS *Saccharomyces c*

PN WO200268693-

06-SEP-2002

[illegible]


```
Percent Similarity: 97.0%      Conservative: 0
Best Local Similarity: 97.0%    Mismatches: 1
Query Match: 24.5%             Indels: 0
DB: 2                           Gaps: 0

US-10-067-832D-1 (1-370) x AAY08414 (1-33)

QY 29 ATGATTGAGTGGTTTTCACAGGACCGCTAGGAAGAAAGTCCGCTTAAGTCGACACC 88
DB 1 MetilegluValValCysAsnAspArgLeuGlyLysLysVal***VallYsCysAsnThr 20

QY 89 GATGACACCATCGGGGACTTGAAGAAACTGATACGGCC 127
DB 21 AspAspThrIleGlyAspLeuLysLysLeuIleAla 33

RESULT 15
ADR43346
ID ADR43346 standard; peptide; 33 AA.
XX AC ADR43346;
XX DT 04-NOV-2004 (first entry)
XX DE Human Beacon protein.
XX KW Beacon; Anorectic; Anabolic; Antidiabetic; Cytostatic; Cardiant;
XX KW Antiinflammatory; Immunosuppressive; Antinfertility; Neuroprotective;
XX KW Nootropic; CLK; myopathy; obesity; anorexia; diabetes; cancer;
XX KW heart disease; inflammation; Alzheimer's; Parkinson's; Pearson Syndrome;
XX KW Pyruvate Carboxylase Deficiency; Pyruvate Dehydrogenase Deficiency;
XX KW Cancer; Acoustic Neuroma; Acute Lymphocytic Leukemia; Carcinoma;
XX KW Leukemia.
XX OS Homo sapiens.
XX PN WO2004069866-A1.
XX PD 19-AUG-2004.
XX PF 10-FEB-2004; 2004WO-AU000147.
XX PR 10-FEB-2003; 2003US-0446191P.
XX PA (AUTO-) AUTOGEN RES PTY LTD.
XX PA (UYDE-) UNIV DEAKIN.
XX PI Collier G, Walder K, Kerr-Bayles L;
XX DR WPI; 2004-604412/58.
XX PT New isolated ligands of mammalian or avian Beacon, useful for e.g.
XX PT preventing or treating disorders associated with myopathy, obesity,
XX PT diabetes, cancer, heart disease, inflammation, or disorders associated
XX PT with the immune system.
XX PS Claim 3; SEQ ID NO 4; 194pp; English.
XX CC The present invention relates to an isolated ligand of mammalian or avian
XX CC Beacon or a homolog or derivative of the Beacon. The composition
XX CC (including the agent capable of modulating the interaction between a
XX CC Beacon and a CLK) or methods are useful for manufacturing a medicament
XX CC for the treatment of a condition characterized by a healthy or unhealthy
XX CC state, including the presence or absence of a disorder associated with
XX CC myopathy, obesity, anorexia, weight maintenance, diabetes, disorders
XX CC associated with mitochondrial dysfunction, genetic disorders, cancer,
XX CC heart disease, inflammation, disorders associated with the immune system,
XX CC infertility, disease associated with the brain and/or metabolic energy
XX CC levels. The disease is selected from Alzheimer's, Parkinson's, diabetes,
XX CC autism, and the aging process. LIC (Lethal Infantile Cardiomyopathy),
XX CC Abgr;-oxidation Defects, Cox Deficiency, Mitochondrial Cytopathy, Alper's
XX CC Disease, Barth syndrome, Carnitine-Acyl-Carnitine Deficiency, Carnitine
XX CC Deficiency, Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II
XX CC Deficiency, Complex III Deficiency, Complex IV Deficiency, Complex V
```

```
CC Deficiency, chronic progressive external ophthalmoplegia syndrome (CPEO),
CC CPT I Deficiency, Glutaric Aciduria Type II, Kearns-Sayre syndrome (KSS),
CC Lactic acidosis, long-chain acyl-CoA dehydrogenase deficiency (LCAD),
CC LCHAD, Leigh Disease, Leber Hereditary Optic Neuropathy (LHON), Luft
CC Disease, mitochondrial DNA depletion, Mitochondrial Encephalopathy,
CC Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase
CC Deficiency, and the other diseases mentioned in the specification. The
CC cancer is selected from ABL1 protooncogene, AIDS Related Cancers,
CC Acoustic Neuroma, Acute Lymphocytic Leukemia, Acute Myeloid Leukemia,
CC Adenocystic carcinoma, Adrenocortical Cancer, Agnogenic myeloid
CC metaplasia, Alopecia, Alveolar soft-part sarcoma, Anal cancer,
CC Angiosarcoma, Aplastic Anemia, Astrocytoma, Ataxia-telangiectasia, Basal
CC Cell Carcinoma (Skin), Bladder Cancer, Bone Cancer, Bowel cancer, Brain
CC Stem Glioma, Brain and CNS Tumours, Breast Cancer, CNS tumours, Carcinoid
CC Tumours, Cervical Cancer, Childhood Brain Tumour, Childhood Cancer,
CC Childood Leukemia, and other cancers mentioned in the specification. The
CC 11 sequences mentioned in the body of the specification do not correspond
XX to the sequences represented in the SEQ ID listing.
```

XX Sequence 33 AA;

Alignment Scores:

Pred. No.:	9.88e-11	Length:	33
Score:	163.00	Matches:	32
Percent Similarity:	97.0%	Conservative:	0
Best Local Similarity:	97.0%	Mismatches:	1
Query Match:	24.5%	Indels:	0
DB:	8	Gaps:	0

US-10-067-832D-1 (1-370) x ADR43346 (1-33)

QY 29 ATGATTGAGTGGTTTTCACAGGACCGCTAGGAAGAAAGTCCGCTTAAGTCGACACC 88

DB 1 MetilegluValValCysAsnAspArgLeuGlyLysLysVal***VallYsCysAsnThr 20

QY 89 GATGACACCATCGGGGACTTGAAGAAACTGATACGGCC 127

DB 21 AspAspThrIleGlyAspLeuLysLysLeuIleAla 33

Search completed: April 7, 2006, 23:39:08

Job time : 161.131 secs

ubiquitin-like protein 8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
C:Accession: S55243; S61068
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
Genetics 139, 921-939, 1995
A:Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like proteins
A:Reference number: S55243; MUID:95229071; PMID:7713442
A:Accession: S55243
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-631 <CAL>
A:Cross-references: UNIPROT:Q39256; UNIPARC:UPI000017A48A; EMBL:L05917
A:Experimental source: ecotype Columbia
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
submitted to the EMBL Data Library, June 1995
A:Reference number: S61068
A:Accession: S61068
A:Molecule type: DNA
A:Residues: 1-341, 'E', 343-631 <CAW>
A:Cross-references: UNIPARC:UPI0000A3588; EMBL:L05917; NID:g870793; PIDN:AAA68879.1; PI
F:73-78/Domain: ubiquitin homology <UBH1>
F:79-154/Domain: ubiquitin homology <UBH2>
F:155-237/Domain: ubiquitin homology <UBH3>
F:238-318/Domain: ubiquitin homology <UBH4>
F:319-392/Domain: ubiquitin homology <UBH5>
F:393-468/Domain: ubiquitin homology <UBH6>
F:469-551/Domain: ubiquitin homology <UBH7>
F:552-627/Domain: ubiquitin homology <UBH8>

Alignment Scores:

Pred. No.:	1.39	Length:	631
Score:	80.00	Matches:	19
Percent Similarity:	58.3%	Conservative:	16
Best Local Similarity:	31.7%	Mismatches:	25
Query Match:	12.0%	Indels:	0
DB:	2	Gaps:	0

US-10-067-832D-1 (1-370) x S55243 (1-631)

Qy	59	GGAAAGAAAGTCGGGTAAAGTGCACACGATGACACATCGGGGACTTGAAGAAACTG	118
Db	561	GlyysThrIleLeuGluValGluSerSerThrIleAlaAsnValysGluys	580
Qy	119	ATAGCGGCCCAACTCGCTCGGGAATGATGCTTCTTAAAGATGGGTACACGATT	178
Db	581	IleGlnValysGluGlyIleLeuProAspGlnMetLeuIlePhePheGlyGlnGln	600
Qy	179	TTTAAGGACCATGATCTCTGGGAGATTATGAATCCAGATGGATGAACCTGGAGCTT	238
Db	601	LeuGluAspGlyValThrLeuGlyAspThrAspIleHisLysLysSerThrLeuTyrl	620

RESULT 6

T03159
large tegument protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03159
R:Enser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: Z14840; MUID:97404659; PMID:9261371
A:Accession: T03159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2606 <ENS>
A:Cross-references: UNIPROT:Q36414; UNIPARC:UPI00000F494A; EMBL:AF005370; NID:g2337967;

Alignment Scores:			
Pred. No.:	3.12	Length:	2606
Score:	77.00	Matches:	32
Percent Similarity:	42.6%	Conservative:	11
Best Local Similarity:	31.7%	Mismatches:	30

Query Match:	11.6%	Indels:	28
DB:	2	Gaps:	6

US-10-067-832D-1 (1-370) x T03159 (1-2606)

Qy	256	TCCCTCTACTGGTAAATAAGCTCCAGGTCATCCCATCGTGATTTTATATCTCCAG	197
Db	1724	AlaProThrGlnProIleTrpLeuGlnValPheProThrValAsp---AenLeuSerMet	1742
Qy	196	AGATACATGGTCCTTAAATAATCGTGACACTT-----TTTAAGAACGATCTT	149
Db	1743	AspTyrlleProIleLysAsnAlaSerProLeuSerLeuGlnValIlePheAsnAenPhe	1762
Qy	148	ATTCAACAGAGTCCAGGTTTGGCGGTATCAGTTTCTTCAAGTCCCGATGGT-----	95
Db	1763	IleGluThr-----TyPheValGlnAlaProGlnGlyProGln	1775
Qy	94	-----GTCATCGGTGTTCACCTTTAACCGCGGACTTT	65
Db	1776	LysAspThrSerGlnTyArgGlySerThrValLeuProAsnValLeuGlnAlaHisPhe	1795
Qy	64	CTTTCCTAGAGCGGTGTTGCAACCCACCTCAATCATTTGGTGGAGCTGTAATCTCTG	5
Db	1796	-----GlyThrIleAlaThrHisLeuIleAsnSerHisTrpAsn---AsnIleLeu	1811
Qy	4	GAA	2
Db	1812	Glu	1812

RESULT 7

T20786
hypothetical protein F11B6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20786
R:Matthews, L.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19324
A:Accession: T20786
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <WLL>
A:Cross-references: UNIPROT:Q9XVQ9; UNIPARC:UPI0000033PF6; EMBL:Z81058; PIDN:CAB02921.1;
C:Experimental source: clone F11B6
C:Genetics:
A:Gene: CESP:F11B6.5
A:Map position: 4
A:Introns: 38/3; 99/1; 183/2; 235/2

Alignment Scores:

Pred. No.:	3.36	Length:	274
Score:	76.50	Matches:	25
Percent Similarity:	41.4%	Conservative:	21
Best Local Similarity:	22.5%	Mismatches:	42
Query Match:	11.5%	Indels:	23
DB:	2	Gaps:	3

US-10-067-832D-1 (1-370) x T20786 (1-274)

Qy	370	TTTTTTTTCGACGATCAAGTTTATTTCATGTAATGTTTAAATGAGCATCTACAA	311
Db	146	TrpTyrlHisAlaLeuThrPheValTyAlaValValThrTySerGluHis-----	163
Qy	310	CAGTGTAAATGACCATCGGAGAGAAAGCAAGTTGGGCAAGGTGGAGGAATTCCT	251
Db	164	-----GlnAlaTrpAlaArgTrpSer-----	170
Qy	250	CTACTGTAATAAGTCCAGTTTCATCCCATCGTGATTTTATATCTCCAGAGATAC	191
Db	171	---LeuAlaLeuAsnLeuAlaValHisThrValMetTyPheTyPheAlaValArgAla	189
Qy	190	ATGTCCTTTAAATCGTGATTCACACTTTTAAAG-----AACGAT	152

Db 190 LeuAasnlleGlnThrProAqProValAlaLysPheIleThrThrIleGlnIleValGln 209
QY 151 CTTATTCCACAGAGTGCAGTTGGGCGGTATCAGATTTCTTCAAGTCCCGATGGTGTC 92
Db 210 PheValIleSerCysTyrrIlePheGlyHisLeuValPheIleLysSerAlaAspSerVal 229
QY 91 ATCGGTGTCACCTTAACGGCGACTTCTTTTCC 59
Db 230 ProGlyCysAlaValSerTrpAsnValLeuSer 240
RESULT 8
T45998
hypothetical protein F9D24.290 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45998
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
A;Accession: T45998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <DAN>
A;Cross-references: UNIPROT:Q9M2H8; UNIPARC:UPI000009B50F; EMBL:AL137081
A;Experimental source: cultivar Columbia; BAC clone F9D24
C;Genetics:
A;Map position: 3
A;Introns: 36/2; 90/1; 170/3
A;Note: F9D24.290
C;Superfamily: Arabidopsis thaliana hypothetical protein F9D24.110
Alignment Scores:
Pred. No.: 5.65 Length: 307
Score: 74.50 Matches: 22
Percent Similarity: 40.8% Conservative: 9
Best Local Similarity: 28.9% Mismatches: 24
Query Match: 11.2% Indels: 21
DB: 2 Gaps: 2
US-10-067-832D-1 (1-370) x T45998 (1-307)
QY 116 CTGATAGCGGCCAAACTGGCACTCGTTGGTAAGATCGTTCTTAAAGTGGTACACG 175
Db 30 LeuIleAla-----GlySerArgTrpArgLeuLeuAlaLeuProLys----- 43
QY 176 ATTTTAAAGACCATGTATCTCTGGGAGATTATGAATCCACGATGGGATGAACCTGGAG 235
Db 44 -----GlyThrAsnTyrGlu 48
QY 236 CTTTATTACCATAGAGGGGAATTCCTCCACCTTGCCCAACCTTGCTTCTCTCCCATG 295
Db 49 PhePheTyrGlnTyrMetGlyValAlaAspSerCysGlnSerLeuThrSerSerTrpArg 68
QY 296 GCTCATTTAAACACTGTGTAGATGCTCATTTTAAACAATTCACATGAA 343
Db 69 ArgHisValLysLeuArgLeuThrIleValAsnGlyIleSerHisLys 84
RESULT 9
B95037
hyaluronidase [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95037
R;Rettiglin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95037
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1066 <KUR>
A;Cross-references: UNIPROT:Q54873; UNIPARC:UPI000012D052; GB:AE005672; PIDN:AAK74491.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0314
Alignment Scores:
Pred. No.: 5.83 Length: 1066
Score: 74.50 Matches: 23
Percent Similarity: 46.3% Conservative: 8
Best Local Similarity: 34.3% Mismatches: 27
Query Match: 11.2% Indels: 9
DB: 2 Gaps: 3
US-10-067-832D-1 (1-370) x B95037 (1-1066)
QY 65 AAAGTCCGGTTAAGTGCACACCGATGACACCATCGGGACTTGAAGAACTGATAGCG 124
Db 128 LysLeuArgPheLysIleLysThrAspAsnLysIleGlyIleAlaLysValArgIleIle 147
QY 125 GCCCAAACTGGC-----ACTCGTTGGAATAAGATCGTT-----CTTAAAAAG 166
Db 148 GluGluSerGlyLysAspLysArgLeuTrpAsnSerAlaThrThrSerGlyThrLysAsp 167
QY 167 TGGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTATGAAATCCACGATGGGATG 226
Db 168 TrpGlnThrIleGluAlaAspTyrSerProThrLeuAspVal-----AspLysIle 184
QY 227 AACCTCGAGCTTTATTACCAG 247
Db 185 LysLeuGluLeuPheTyrGlu 191
RESULT 10
F97907
hyaluronate lyase (EC 4.2.2.1) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F97907
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F97907
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1078 <KUR>
A;Cross-references: UNIPROT:Q8CWU3; UNIPARC:UPI00000E4928; GB:AE007317; PIDN:AAK99090.1;
C;Genetics:
A;Gene: hysA
C;Keywords: carbon-oxygen lyase
Alignment Scores:
Pred. No.: 7.55 Length: 1078
Score: 73.50 Matches: 22
Percent Similarity: 46.3% Conservative: 9
Best Local Similarity: 32.8% Mismatches: 27
Query Match: 11.1% Indels: 9
DB: 2 Gaps: 3
US-10-067-832D-1 (1-370) x F97907 (1-1078)
QY 65 AAAGTCCGGTTAAGTGCACACCGATGACACCATCGGGACTTGAAGAACTGATAGCG 124
Db 140 LysLeuArgPheLysIleLysThrAspAsnLysValGlyIleAlaLysValArgIleIle 159
QY 125 GCCCAAACTGGC-----ACTCGTTGGAATAAGATCGTT-----CTTAAAAAG 166
Db 160 GluGluSerGlyLysAspLysArgLeuTrpAsnSerAlaThrThrSerGlyThrLysAsp 179
QY 167 TGGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTATGAAATCCACGATGGGATG 226

Db 180 TrpGlnThrIleGluAlaAspTyrSerProThrLeuAspVal-----AspLysIle 196
Qy 227 AACCTGGAGCTTTATTACCAG 247
Db 197 LysLeuGluLeuPheTyrGlu 203
RESULT 11
S60529
envelope polyprotein gp1 - human immunodeficiency virus type 1 (isolate CI-14-13) (frag
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate CI-14-13
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S60529
R;Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A;Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A;Reference number: S60521; MUID:94280700; PMID:8011235
A;Accession: S60529
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-299 <JAN>
A;Cross-references: UNIPROT:Q76172; UNIPARC:UPI000010385B; EMBL:X72031; NID:G468637; PID
A;Experimental source: isolate CI-14-13
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein
Alignment Scores:
Pred. No.: 9.48 Length: 299
Score: 72.50 Matches: 28
Percent Similarity: 40.4% Conservative: 12
Best Local Similarity: 28.3% Mismatches: 26
Query Match: 10.9% Indels: 33
DB: 2 Gaps: 4
US-10-067-832D-1 (1-370) x S60529 (1-299)
Qy 5 CAGGAGATTACAGCTCCAGCCACCAATGATTGAGTGTTGCAACGACCGCTAGGAAG 64
Db 8 GluAsnIleThrAsnAsnAlaLysThrIleVal-----GlnLeuValLys 23
Qy 65 AAAGTCGCGTTAAGTCAAC----- 85
Db 24 ProValArgIleAsnCysThrArgProSerAsnAsnThrArgLysSerValProIleGly 43
Qy 86 -----ACCGATGACACCATCGGACTTGAGAACTGATAGCG 124
Db 44 ProGlyGlnAlaPheTyrAlaThrAspAspIleIleGlyAspIleArgGlnAlaHisCys 63
Qy 125 GCCCAAACTGGCACTCGTTGGAATAAGATCGTT-----CTTAAAG 166
Db 64 AsnValSerLysThrGluTrpAsnGluThrLeuArgGlnValAlaThrGlnLeuLysLys 83
Qy 167 TGGTAC-----ACGATTTTAAAGACCATGATCTCTGGAGATTATGAATC 214
Db 84 HisPheLysAsnAlaThrIleIlePheAlaAsnProSerGlyGlyAspLeuGluVal 102
RESULT 12
S60528
envelope polyprotein gp1 - human immunodeficiency virus type 1 (isolate CI-14-5 and iso
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate CI-14-5; isolate CI-14-21
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S60528; S60530
R;Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A;Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A;Reference number: S60521; MUID:94280700; PMID:8011235
A;Accession: S60528
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-299 <JAN>
A;Cross-references: UNIPROT:Q76171; UNIPARC:UPI0000101A6F; EMBL:X72030; PIDN:CAAS0915.1; PI
A;Experimental source: isolate CI-14-5
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
A;Accession: S60530
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-299 <JAN>
A;Cross-references: UNIPARC:UPI0000101A6F; EMBL:X72032; NID:G468639; PIDN:CAAS0915.1; PI
A;Experimental source: isolate CI-14-21
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein
Alignment Scores:
Pred. No.: 9.48 Length: 299
Score: 72.50 Matches: 28
Percent Similarity: 40.4% Conservative: 12
Best Local Similarity: 28.3% Mismatches: 26
Query Match: 10.9% Indels: 33
DB: 2 Gaps: 4
US-10-067-832D-1 (1-370) x S60528 (1-299)
Qy 5 CAGGAGATTACAGCTCCAGCCACCAATGATTGAGTGTTGCAACGACCGCTAGGAAG 64
Db 8 GluAsnIleThrAsnAsnAlaLysThrIleVal-----GlnLeuValLys 23
Qy 65 AAAGTCGCGTTAAGTCAAC----- 85
Db 24 ProValArgIleAsnCysThrArgProSerAsnAsnThrArgLysSerValProIleGly 43
Qy 86 -----ACCGATGACACCATCGGACTTGAGAACTGATAGCG 124
Db 44 ProGlyGlnAlaPheTyrAlaThrAspAspIleIleGlyAspIleArgGlnAlaHisCys 63
Qy 125 GCCCAAACTGGCACTCGTTGGAATAAGATCGTT-----CTTAAAG 166
Db 64 AsnValSerLysThrGluTrpAsnGluThrLeuArgGlnValAlaThrGlnLeuLysLys 83
Qy 167 TGGTAC-----ACGATTTTAAAGACCATGATCTCTGGAGATTATGAATC 214
Db 84 HisPheLysAsnAlaThrIleIlePheAlaAsnProSerGlyGlyAspLeuGluVal 102
RESULT 13
H84984
bo-type ubiquinol oxidase (EC 1.10.3.-) chain I [similarity] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 10-May-2001
C;Accession: H84984
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A.
A;Reference number: H84930; MUID:20445173; PMID:10993077
A;Accession: H84984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-662 <STO>
A;Cross-references: UNIPARC:UPI000005E5C3; GB:AP0000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: cyoB; BU471
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated complex
F;106,421/Binding site: heme a iron (His) (axial ligands) #status predicted
F;284-288/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F;288/Binding site: oxygen (Tyr) #status predicted
Alignment Scores:
Pred. No.: 16.2 Length: 662

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:32:23 ; Search time 34.178 Seconds
(without alignments)
1527.566 Million cell updates/sec

Title: US-10-067-832D-1

Perfect score: 665

Sequence: 1 gttccaggagattacagctc.....tttgatctgcacaaaaaaa 370

Scoring table:

BLSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Dgapop 6.0 , Dext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB spool/US10067832/runat_07042006_175611_9700/app query.fasta_1
-DB=Uniprot -OPMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -SPART=1 -END=-1 -NATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10067832 @CGN_1_580 @runat_07042006_175611_9700 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	59.2	73	1 UBL5 HUMAN	Q9bz11 homo sapien
2	394	59.2	73	1 UBL5 MESAU	O5egx7 mesocricetu
3	394	59.2	73	1 UBL5 MOUSE	O9epv8 mus musculus
4	394	59.2	73	1 UBL5_PSAOB	Q791b0 psammomyes o
5	394	59.2	73	2 QSRC10_FONPY	Q5rc10 pongo pygma
6	394	59.2	73	2 Q4R5J3_MACFA	Q4r5j3 macaca fasc
7	368	55.3	73	1 UBL5 BRARE	Q7sxf2 brachydanio
8	367	55.2	73	2 Q5HZC1_XENLA	Q5hzc1 xenopus lae
9	354	53.2	73	2 Q4SM16_TETNG	Q4sm16 tetraodon n
10	344	51.7	73	2 Q7QHW2_ANOGA	Q7qhw2 anopheles g
11	339	51.0	73	1 UBL5_DROME	Q9v998 drosophila
12	331	49.8	73	1 UBL5_CABEL	P91302 caenorhabdi
13	331	49.8	73	2 Q617M9_CAEBR	Q617m9 caenorhabdi
14	329	49.5	73	2 Q5BS57_SCHJA	Q5bs57 schistosoma
15	325	48.9	73	2 Q4VAF8_MOUSE	Q4vaf8 mus musculus
16	315	47.4	73	2 Q6K220_ORYSA	Q6k220 oryza sativ

17	313	47.1	73	1 UBL5_ARATH	Q9fgz9 arabidopsis
18	313	47.1	73	2 Q570V8_ARATH	Q570v8 arabidopsis
19	308	46.3	73	2 Q7RBM4_PLAYO	Q7rbm4 plasmodium
20	308	46.3	73	2 Q4YUJ7_PLABE	Q4yuj7 plasmodium
21	306	46.0	73	2 Q9M1U1_ARATH	Q9m1u1 arabidopsis
22	302	45.4	73	2 Q81545_PLAF7	Q81545 plasmodium
23	301	45.3	73	1 HUB1_SCHPO	Q94650 schizosacch
24	293	44.1	73	2 Q4MZ69_THEPA	Q4mz69 theileria p
25	291	43.8	76	2 Q4UBS9_CRYNE	Q4ubes9 theileria a
26	288	43.3	276	2 Q55M54_CRYNE	Q55m54 cryptococcu
27	288	43.3	276	2 Q5K8L5_CRYNE	Q5k8l5 cryptococcu
28	266	40.0	73	1 HUB1_D8HA	Q6bup7 debaromyces
29	263	39.5	70	2 Q6CI04_YARLI	Q6ci04 yarrowia li
30	250	37.6	47	2 Q5BJS1_RAT	Q5bj81 rattus norv
31	248	37.3	73	1 HUB1_YEAST	Q6q546 saccharomyc
32	243	36.5	73	1 HUB1_CANGA	Q6f1x7 candida gla
33	238.5	35.9	74	1 HUB1_KLJLA	Q6cu12 kluyvaromyc
34	238.5	35.9	79	2 Q6CU11_KLJLA	Q6cu11 kluyvaromyc
35	235	35.3	73	1 HUB1_ASHGO	Q756x3 ashbya gos
36	231	34.7	87	2 Q54Q03_DICDI	Q54q03 dictyosteli
37	218	32.8	79	2 Q50P03_ENTHI	Q50p03 entamoeba h
38	168	25.3	73	2 Q4P9W2_USTMA	Q4p9w2 ustilago ma
39	154.5	23.2	237	2 Q4I016_GIBZE	Q4i016 gibberella
40	141.5	21.3	616	2 Q5BCG2_SWENI	Q5bcg2 aspergillus
41	129.5	19.5	239	2 Q526Z0_MAGGR	Q526z0 magnaporthe
42	119.5	18.0	261	2 Q8X065_NEUCR	Q8x065 neurospora
43	116	17.4	189	2 Q4WYK6_ASPFU	Q4wyk6 aspergillus
44	98.5	14.8	851	2 Q7ZMI4_9HIV1	Q7zmi4 human immun
45	95.5	14.4	115	2 Q7ZCU2_9HIV1	Q7zcu2 human immun

ALIGNMENTS

RESULT 1
ID UBL5_HUMAN
AC Q9BZL1; STANDARD; PRT; 73 AA.
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=UBL5;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=iris;
RX MEDLINE=21100898; PubMed=1161819; DOI=10.1006/geno.2000.6439;
RA Friedman J.S., Koop B.F., Raymond V., Walter M.A.,
RT "Isolation of a ubiquitin-like (UBL5) gene from a screen identifying
RT highly expressed and conserved iris genes.";
RL Genomics 71:252-255(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.,
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ubiquitin-like protein 5.
 GN Name=UBI5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney, Pancreas, Spinal ganglion, and Tongue;
 RX MEDLINE=22354681; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Gutentich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Negashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verdardo R., Wagner L., Wallesstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AK002730; BAB22312.1; -; mRNA.
 DR EMBL; AK003992; BAB23111.1; -; mRNA.
 DR EMBL; AK007726; BAB25215.1; -; mRNA.
 DR EMBL; AK009854; BAB26545.1; -; mRNA.
 DR EMBL; AK012803; BAB28481.1; -; mRNA.
 DR EMBL; AK051149; BAC34537.1; -; mRNA.
 DR EMBL; BC028498; AAC28498.1; -; mRNA.
 DR PDB; 1UH6; NMR; A=1-73.
 DR MGI; MGI:1913427; Ubl5.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS00299; UBIQUITIN 1; FALSE NEG.
 DR PROSITE; PS0053; UBIQUITIN 2; FALSE NEG.
 KW 3D-structure; Ubl conjugation pathway.
 FT DOMAIN 1 73 Ubiquitin-like.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;
 Alignment Scores:
 Pred. No.: 1.03e-37 Length: 73
 Score: 394.00 Matches: 73
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 59.2% Indels: 0
 DB: 1 Gaps: 0
 US-10-067-832D-1 (1-370) x UBL5_MOUSE (1-73)
 QY 29 ATGATTCAGTGGTTCACAGCAGCTCTAGGAAGAAGTCCGCTTAAGTCGACACACC 88
 DB 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 20
 QY 89 GATCACACCATCGGGGACTTGAAGAACTGATACGCCCAACTGGCACCTCGTTGGAAAT 148
 DB 21 AspAspThrileGlyAspLeuLysLysLysLysLysLysLysLysLysLysLysLys 40
 QY 149 ARGATCGTCTTAAAAAGTGGTACACGATTTTAAAGACCATGATCTCTCGGAGATPAT 208
 DB 41 LysileValLeuLysLysTrpTrpThrilePheLysAspHisValSerLeuGlyAspTyr 60
 QY 209 GAATCCAGCATGGATGACCTGGAGCTTATTACCAG 247
 DB 61 GlulleHisAspGlyMetAsnLeuGluLeuTyrTrpGln 73
 RESULT 4
 UBL5_PSAOB STANDARD; PRT; 73 AA.
 ID _UBL5_PSAOB
 AC Q791B0;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ubiquitin-like protein 5 (Beacon protein).
 GN Name=UBL5;
 OS Psammomyes obesus (Fat sand rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Gerbillinae; Psammomyes.
 OX NCBI_TaxID=48139;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=20527879; PubMed=11078442;
 RA Collier G.R., McMillan J.S., Windmill K., Walder K., Tenne-Brown J.,
 RA de Silva A., Trevaaskis J., Jones S., Morton G.J., Lee S., Augert G.,
 RA Civitarese A., Zimmet P.Z.;
 RT "Beacon: a novel gene involved in the regulation of energy balance.";
 RL Diabetes 49:1766-1771(2000).
 CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC

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CC EMBL; AF318186; AAC34704.1; -; mRNA.
 CC SNR; Q791B0; 1-73.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
 DR PROSITE; PS50053; UBIQUITIN_2; FALSE_NEG.
 KW Ubl conjugation pathway.
 FT DOMAIN 1 73 Ubiquitin-like.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
 Pred. No.: 1.03e-37 Length: 73
 Score: 394.00 Matches: 73
 Percent Similarity: 100.0% Conservativeness: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 59.2% Indels: 0
 DB: 1 Gaps: 0

US-10-067-832D-1 (1-370) x UBL5_PSAOB (1-73)

QY 29 ATGATTGAGTGGTTTTCGACAGCGCTCTAGGAAGAAAGTCCGCTTAAGTCAACACC 88
 |||||
 Db 1 MetileGluValValCysAenAspArgLeuGlyLysValArgVallysCysAenThr 20
 |||||
 QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
 |||||
 Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTTPAen 40
 |||||
 QY 149 AAGATCGTTCTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
 |||||
 Db 41 LysileValLeuLysLysTrpTyThrIlePheLysAspHisValSerLeuGlyAspTyr 60
 |||||
 QY 209 GAAATCCAGCATGGGATGAACCTGGAGCTTTATTACCAG 247
 |||||
 Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73
 |||||

RESULT 5

QSRCIO_PONPY
 ID QSRCIO_PONPY PRELIMINARY; PRT; 73 AA.
 AC QSRCIO;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKF2p469G145.
 GN Names=DKF2p469G145;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG The German cDNA Consortium;
 RA Ansoerge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
 RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR858290; CAH90527.1; -; mRNA.
 DR SNR; Q5RCIO; 1-73.
 DR GO; GO:0006464; P:protein modification; IEA.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
 Pred. No.: 1.03e-37 Length: 73

Score: 394.00 Matches: 73
 Percent Similarity: 100.0% Conservativeness: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 59.2% Indels: 0
 DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x QSRCIO_PONPY (1-73)

QY 29 ATGATTGAGTGGTTTTCGACAGCGCTCTAGGAAGAAAGTCCGCTTAAGTCAACACC 88
 |||||
 Db 1 MetileGluValValCysAenAspArgLeuGlyLysValArgVallysCysAenThr 20
 |||||
 QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
 |||||
 Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTTPAen 40
 |||||
 QY 149 AAGATCGTTCTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
 |||||
 Db 41 LysileValLeuLysLysTrpTyThrIlePheLysAspHisValSerLeuGlyAspTyr 60
 |||||
 QY 209 GAAATCCAGCATGGGATGAACCTGGAGCTTTATTACCAG 247
 |||||
 Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73
 |||||

RESULT 6

Q4R5J3_MACFA
 ID Q4R5J3_MACFA PRELIMINARY; PRT; 73 AA.
 AC Q4R5J3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Brain cDNA, clone: OFIA-12296, similar to human ubiquitin-like 5 (UBL5), (Testis cDNA, clone: QrsA-15893, similar to human ubiquitin-like 5 (UBL5)).
 DE Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopitheciniae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis; its
 RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications."
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs."
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB169550; BAE01632.1; -; mRNA.
 DR EMBL; AB169933; BAE01034.1; -; mRNA.
 SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
 Pred. No.: 1.03e-37 Length: 73
 Score: 394.00 Matches: 73
 Percent Similarity: 100.0% Conservativeness: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 59.2% Indels: 0
 DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x Q4R5J3_MACFA (1-73)

QY 29 ATGATTGAGTGGTTTTCGACAGCGCTCTAGGAAGAAAGTCCGCTTAAGTCAACACC 88
 |||||
 Db 1 MetileGluValValCysAenAspArgLeuGlyLysValArgVallysCysAenThr 20
 |||||
 QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
 |||||
 Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTTPAen 40
 |||||


```
QY 149 AAGATCGTCTTAAAGCTGGTACACGATTTTAAAGGACCATGTATCTCTGGAGATTAT 208
Db |||||||
QY 41 LysileValLeuLysLysTrpTrpThrilePheLysAspHisValSerLeuGlyAspTyr 60
Db |||||||

QY 209 GAAATCCACGATGGGATCAACTGGAGCTTTATTACCAG 247
Db 61 GlulleHisAspGlyMetAsnLeuGluLeuTyrGln 73

RESULT 7
ID UBL5_BRARE STANDARD; PRT; 73 AA.
AC Q7SKF2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=ubl5; ORFNames=zgc:66388;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BC055630; AAH55630.1; -; mRNA.
DR SRR; Q7SKF2; 1-72.
DR ZFIN; ZDB-GENE-040426-1629; zgc:66388.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS50053; UBIQUITIN_2; FALSE_NEG.
KW Ubiquitin conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8587 MW; 23716CBB0FC7C545 CRC64;

Alignment Scores:
Pred. No.: 1.31e-34 Length: 73
Score: 368.00 Matches: 68
Percent Similarity: 97.2% Conservative: 2
Best Local Similarity: 94.4% Mismatches: 2
Query Match: 55.3% Indels: 0
DB: 1 Gaps: 0

US-10-067-832D-1 (1-370) x UBL5_BRARE (1-73)

QY 29 ATGATTGAGTGGTGTTCACACGACCGTCTAGGAAGAAAGTCGCGTTAAGTGCACAC 88
Db |||||||
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGGCCTCGTTGGAAT 148
Db ::|||
QY 21 GluAspThrileGlyAspLeuLysLeuileAlaGlnThrGlyThrArgTrpGlu 40
Db |||||||
QY 149 AAGATCGTCTTAAAGCTGGTACACGATTTTAAAGGACCATGTATCTCTGGAGATTAT 208
Db |||||||
QY 41 LysileValLeuLysLysTrpTrpThrilePheLysAspHisValSerLeuGlyAspTyr 60
Db |||||||

QY 209 GAAATCCACGATGGGATCAACTGGAGCTTTATTACCAG 244
Db 61 GlulleHisAspGlyMetAsnLeuGluLeuTyrTyr 72
```

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RESULT 8
QSHZC1_XENLA PRELIMINARY; PRT; 73 AA.
AC QSHZC1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplaton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089084; AAH89084.1; -; mRNA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8635 MW; 2A51E123F36FF390 CRC64;

Alignment Scores:
Pred. No.: 1.73e-34 Length: 73
Score: 367.00 Matches: 67
Percent Similarity: 97.3% Conservative: 4
Best Local Similarity: 91.8% Mismatches: 2
Query Match: 55.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x QSHZC1_XENLA (1-73)

QY 29 ATGATTGAGTGGTGTTCACACGACCGTCTAGGAAGAAAGTCGCGTTAAGTGCACAC 88
Db |||||||
QY 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnSer 20
```

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QY 89 GATGACACCATCGGGGACTTGAAGAAACTGATAGCGCCCAAACTGCGACTCGTTGGAAAT 148
|||||
Db 21 AspAspThrIleLysAspLeuLysLeuIleAlaAlaGlnThrGlyThrArgTyrAsp 40
|||||
QY 149 AAGATCGTTCTTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGAGATTAT 208
|||||
Db 41 LysValValLeuLysLysTyrThrIlePheLysAspHisValThrLeuSerAspTyr 60
|||||
QY 209 GAATCCACGATCGGATGAACCTGGAGCTTTATTACCAG 247
|||||
Db 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73
|||||
RESULT 9
Q4SMI6_TETNG
ID Q4SMI6_TETNG PRELIMINARY; PRT; 73 AA.
AC Q4SMI6;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome 18 SCAP14547, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00015743001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Bilemont C., Skalli Z., Cattelico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014547; 73
DR NON TER 73
SQ SEQUENCE 73 AA; 8592 MW; 6A1CA0323F8E8EB CRC64;

Alignment Scores:
Pred. No.: 6.15e-33 Length: 73
Score: 354.00 Matches: 66
Percent Similarity: 95.9% Conservative: 4
Best Local Similarity: 90.4% Mismatches: 3
Query Match: 53.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x Q4SMI6_TETNG (1-73)
QY 29 ATGATTGAGTGGTTTTCACACGACCGCTTAGGAAAGAAAGTCCGCGTTAAGTCAACACC 88
|||||
Db 1 MetIleGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnPro 20
|||||
QY 89 GATGACACCATCGGGGACTTGAAGAAACTGATAGCGCCCAAACTGCGACTCGTTGGAAAT 148
|||||
Db 21 GlnAspSerIleGlyAspLeuLysLysLeuIleAlaAlaGlnThrGlyThrArgTyrAsp 40
|||||
RESULT 11
UBI5_DROME
```

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QY 149 AAGATCGTTCTTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGAGATTAT 208
|||||
Db 41 LysValValLeuLysLysTyrThrIlePheLysAspHisValThrLeuSerAspTyr 60
|||||
QY 209 GAATCCACGATCGGATGAACCTGGAGCTTTATTACCAG 247
|||||
Db 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73
|||||
RESULT 10
Q7QHM2_ANOGA
ID Q7QHM2_ANOGA PRELIMINARY; PRT; 73 AA.
AC Q7QHM2;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE ENSANGP00000015674.
GN ORFNames=ENSANGG00000013185;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA The Anopheles gambiae Sequence Committee;
RC STRAIN=PEST;
RG "Anopheles gambiae re-annotation."
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05206.2; -; Genomic_DNA.
DR SNR; Q7QHM2; 1-73.
DR GO; GO:006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; P850053; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8599 MW; 43D212BE601B3C0D CRC64;

Alignment Scores:
Pred. No.: 9.6e-32 Length: 73
Score: 344.00 Matches: 61
Percent Similarity: 94.5% Conservative: 8
Best Local Similarity: 83.6% Mismatches: 4
Query Match: 51.7% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x Q7QHM2_ANOGA (1-73)
QY 29 ATGATTGAGTGGTTTTCACACGACCGCTTAGGAAAGAAAGTCCGCGTTAAGTCAACACC 88
|||||
Db 1 MetLeuGluIleThrCysAsnAspArgLeuGlyLysValArgValLysCysAsnPro 20
|||||
QY 89 GATGACACCATCGGGGACTTGAAGAAACTGATAGCGCCCAAACTGCGACTCGTTGGAAAT 148
|||||
Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaAlaGlnThrGlyThrArgTyrAsp 40
|||||
QY 149 AAGATCGTTCTTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGAGATTAT 208
|||||
Db 41 LysValValLeuLysLysTyrThrIlePheLysAspHisValThrLeuSerAspTyr 60
|||||
QY 209 GAATCCACGATCGGATGAACCTGGAGCTTTATTACCAG 247
|||||
Db 61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73
|||||
RESULT 11
UBI5_DROME
```

ID UBL5 DROME STANDARD; PRT; 73 AA.
 AC Q9V998; Q9V998; 73 AA.
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ubiquitin-like protein 5.
 GN Name=1(2)K03203; ORFNames=CG3450;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.I., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lakso P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Rittington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasmann D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Berkeley;
 RA Stapleton M., Carlson J.W., Chavez C., Friese E., George R.A.,
 RA Pacle J.M., Park S., Wan K.H., Yu C., Celisner S.E.,
 RA Submitted (JUN-2005) to the ENBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AE003790; AAF57398.1; -; Genomic_DNA.
 DR EMBL; BT023690; AAY85090.1; -; mRNA.
 DR SMR; Q9V998; 1-73.
 DR Ensembl; CG3450; Drosophila melanogaster.
 DR FlyBase; FBgn0022224; l(2)k03203.
 DR GO; GO:0005737; C:cytoplasm; ISS.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; Ubiquitin; 1.
 DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
 DR PROSITE; PS0053; UBIQUITIN_2; 1.
 KW Ubl conjugation pathway.
 FT DOMAIN 1 73 Ubiquitin-like.
 SQ SEQUENCE 73 AA; 8570 MW; 0870111AC586A70 CRC64;
 Alignment Scores:
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 Score: 339.00 Matches: 63
 Percent Similarity: 90.4% Conservative: 3
 Best Local Similarity: 86.3% Mismatches: 7
 Query Match: 51.0% Indels: 0
 DB: 1 Gaps: 0
 US-10-067-832D-1 (1-370) x UBL5_DROME (1-73)
 QY 29 ATGATTGAGTGGTTCACACGCGCTAGAGAAAGAAAGTCCGGTTAAGTGCAACACC 88
 DB 1 MetileglutThrCysAsnAspArgLeuGlyLysValArgValLysCysAsnPro 20
 QY 89 GATGACACCATCGGGAGCTGGAAGAACTGATAGCGGCCCAACTGGCAGCTCGTTGGAA 148
 DB 21 AspAspThrileGlyAspLeuLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 QY 149 AAGATCGCTTCTTAAAGAGTGTACACCATGTTTAAAGGACCATGATCTCTCGGAGATTAT 208
 DB 41 LysileValleuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
 QY 209 GAAATCCACCATGGATGCAACCTCGAGCTTTATTACCAG 247
 DB 61 GlulleHisepGlyMetAsnLeuLeuTyrrGln 73
 RESULT 12
 UBL5 CAEEL
 ID UBL5 CAEEL STANDARD; PRT; 73 AA.
 AC P91302;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ubiquitin-like protein 5.
 GN Name=ubl-5; ORFNames=F46F11.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RT "Genome sequencing consortium;
 RT investigating biology";
 RL Science 282:2012-2018 (1998).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
DR EMBL; U88173; AAK21382.1; -; Genomic_DNA.
DR PIR; T25763; T25763.
DR SMR; P91302; 1-73.
DR Ensemble; F46F11.4; Caenorhabditis elegans.
DR WormBase; WBGene0006726; ubi-5.
DR WormPepp; F46F11.4; CE10602.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
KW Complete proteome; Ubi conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8738 MW; 61CA839BBA4006A4 CRC64;

Alignment Scores:
Pred. No.: 3.42e-30 Length: 73
Score: 331.00 Matches: 59
Percent Similarity: 89.0% Conservative: 6
Best Local Similarity: 80.8% Mismatches: 8
Query Match: 49.8% Indels: 0
DB: 1 Gaps: 0

US-10-067-832D-1 (1-370) x UBL5_CAEEL (1-73)

QY 29 ATGATTGAGGTGGTTTGCACACCGCTCTAGGAAGAAAGTCCGCTTAAGTGCACACC 88
DB 1 MetileGluileThrValAsnAspArgLeuGlyLysLysValArgileLysCysAsnPro 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGCACTCGTTGGAAT 148
DB 21 SerAspThrileGlyAspLeuLysLysLeuileAlaAlaGlnThrGlyThrArgTprGlu 40
QY 149 AAGATCGTTCTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
DB 41 LysileValleuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
QY 209 GAAATCCACGATGGGATGACCTGGAGCTTTATTACCAG 247
DB 61 GluileHisGluGlyPheAsnPheGluLeuTyrTyrGln 73

RESULT 13

Q617M9 CAEBR
ID Q617M9 CAEBR PRELIMINARY; PRT; 73 AA.
AC Q617M9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG14905.
GN Name=CBG14905;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000068; CAE68926.1; -; Genomic_DNA.
DR SMR; Q617M9; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
KW Hypothetical protein.

SQ SEQUENCE 73 AA; 8738 MW; 61CA839BBA4006A4 CRC64;

Alignment Scores:

Pred. No.: 3.42e-30 Length: 73
Score: 331.00 Matches: 59
Percent Similarity: 89.0% Conservative: 6
Best Local Similarity: 80.8% Mismatches: 8
Query Match: 49.8% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x Q617M9_CAEER (1-73)

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DB 21 SerAspThrileGlyAspLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 40
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DB 41 LysileValleuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
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Q5BS57 SCHJA
ID Q5BS57 SCHJA PRELIMINARY; PRT; 73 AA.
AC Q5BS57
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoida; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Han Z.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY915407; AAX30628.1; -; mRNA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8679 MW; D3A862289A087CB5 CRC64;

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Best Local Similarity: 79.5% Mismatches: 8
Query Match: 49.5% Indels: 0
DB: 2 Gaps: 0

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QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGCACTCGTTGGAAT 148
DB 21 ThrAspLysValSerAspLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 40
QY 149 AAGATCGTTCTTAAAAAGTGGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
DB 41 ArgileValleuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
QY 209 GAAATCCACGATGGGATGACCTGGAGCTTTATTACCAG 247
DB 61 GluileAsnAspGlyMetAsnLeuGluLeuTyrTyrGln 73

Search completed: April 7, 2006, 23:46:28
Job time : 171.89 secs

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AC Q4VAF8;
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DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCHI_taxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC096400; AAH96400.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8582 MW; 9B2C9977752A6068 CRC64;

Alignment Scores:
Pred. No.: 1.78e-29 Length: 73
Score: 325.00 Matches: 61
Percent Similarity: 86.3% Conservative: 2
Best Local Similarity: 83.6% Mismatches: 10
Query Match: 48.9% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x Q4VAF8_MOUSE (1-73)
Qy 29 ATGATTGAGTGGTGTTCGACGACCGCTCTAGCAAGAAAGTCGCGTTTAAGTCAACACC 88
Db 1 MetThrGluValValCysAsnTyrHisLeuGlyLysLysValHisValLysTyrAsnThr 20
Qy 89 GATGACACCACTCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuIleGluAlaGlnThrGlyThrHisTyrAsn 40
Qy 149 AAGATCGTCTTAARAAGTGGTACGACGATTTTAAAGGACCATGATCTCTGGGAGATTAT 208
Db 41 LysIleIleLysLysLysTyrThrPheLeuGlnAspHisValSerLeuGlyAspTyr 60
Qy 209 GAAATCCACCATGGGATCAACCTGGAGCTTTATTATACCAG 247
Db 61 GluIleHisaspGlyMetAsnLeuGluLeuSerTyrGln 73
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GenCore version 5.1.7
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	394	59.2	73	2	US-09-331-930A-21
5	370	55.6	73	2	US-09-331-930A-24
6	354	53.2	73	2	US-09-331-930A-25
7	331	49.8	73	2	US-09-331-930A-22
8	286	43.0	66	2	US-09-331-930A-23
9	252	37.9	75	2	US-09-248-796A-16302
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24	66	9.9	110	2	US-08-252-991A-25531
25	66	9.9	653	2	US-08-849-602C-27
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28	65.5	9.8	102	2	US-09-732-210-1289
29	65.5	9.8	312	2	US-09-114-001C-3534
30	65.5	9.8	312	2	US-09-710-279-3104
31	65.5	9.8	502	2	US-09-540-236-1922
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35	65	9.8	533	2	US-09-252-991A-21407
36	64.5	9.7	281	2	US-09-248-796A-20512
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39	64	9.6	214	1	US-08-916-902A-3
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ALIGNMENTS

RESULT 1

US-09-331-930A-2
; Sequence 2, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-2007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-2

Alignment Scores:			
Pred. No.:	2,48e-45	Length:	73
Score:	394.00	Matches:	73
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	59.2%	Indels:	0
DB:	2	Gaps:	0

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Db 1 MetileGluValValCysAenAspArgLeuGlyLysValArgValLysCysAenThr 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrileGlyAspLeuLysLysLeuilealaalaglnThrGlyThrArgTrpAsn 40
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RESULT 2
US-09-331-930A-19
; Sequence 19, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Unknown Organism
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-19
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Pred. No.: 2,48e-45 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 2 Gaps: 0
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QY 29 ATGATTGAGTGGTTTCACAGCCGCTAGGAAAGAAAGTCCGCGTTAAGTGCACACC 88
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QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
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; GENERAL INFORMATION:
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; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Unknown Organism
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-19
Alignment Scores:
Pred. No.: 2,48e-45 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 2 Gaps: 0
US-10-067-832D-1 (1-370) x US-09-331-930A-19 (1-73)
QY 29 ATGATTGAGTGGTTTCACAGCCGCTAGGAAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValCysAenAspArgLeuGlyLysValArgValLysCysAenThr 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrileGlyAspLeuLysLysLeuilealaalaglnThrGlyThrArgTrpAsn 40
QY 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValleuLysLysTrpTyThrilePhelysAspHisValSerLeuGlyAspTyr 60
QY 209 GAAATCCACGATGGGATGAACCTGGAGCTTTATTACCAG 247
Db 61 GluileHisaspGlyMetAenLeuGluLeuTyrTrgln 73
RESULT 4
US-09-331-930A-21
; Sequence 21, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Murine sp.
```


US-09-331-930A-21

Alignment Scores:

Pred. No.: 2.48e-45 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-21 (1-73)

Qy 29 ATGATTGAGTGGTTTCACACGCGCTAGGAAGAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAAT 148
Db 21 AspaAspThrileGlyAspLeuLysLeuilealaalaglnThrGlyThrArgTrpAsn 40
Qy 149 AAGATCGTTCTTAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValLeuLysLysTrpTyThrilePheLysAspHisValSerLeuGlyAspTy 60
Qy 209 GAATCCACGATGGATCAACCTGAGCTTTATTACCAG 247
Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyTrpGln 73

RESULT 5

US-09-331-930A-24

; Sequence 24, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa

US-09-331-930A-24

Alignment Scores:
Pred. No.: 4.95e-42 Length: 73
Score: 370.00 Matches: 67
Percent Similarity: 97.2% Conservative: 3
Best Local Similarity: 93.1% Mismatches: 2
Query Match: 55.6% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-24 (1-73)

Qy 29 ATGATTGAGTGGTTTCACACGCGCTAGGAAGAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAAT 148
Db 21 AspaAspThrileGlyAspLeuLysLeuilealaalaglnThrGlyThrArgTrpAsn 40
Qy 149 AAGATCGTTCTTAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208

Db 41 LysileValLeuLysLysTrpTyThrileTyTrLysAspHisileThrLeuAlaAspTy 60
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluileHisAspGlyMetGlyLeuGluLeuTyTr 72

RESULT 6

US-09-331-930A-25
; Sequence 25, Application US/09331930A
; Patent No. 6436670

; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

US-09-331-930A-25

Alignment Scores:
Pred. No.: 7.86e-40 Length: 73
Score: 354.00 Matches: 65
Percent Similarity: 93.1% Conservative: 2
Best Local Similarity: 50.3% Mismatches: 5
Query Match: 53.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-25 (1-73)

Qy 29 ATGATTGAGTGGTTTCACACGCGCTAGGAAGAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAAT 148
Db 21 AspaAspThrileGlyAspLeuLysLeuilealaalaglnThrGlyThrArgTrpAsn 40
Qy 149 AAGATCGTTCTTAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValLeuLysLysTrpTyThrileTyTrLysAspHisileThrLeuAlaAspTy 60
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluValHisAspGlnThrAsnLeuGluLeuTyTr 72

RESULT 7

US-09-331-930A-22
; Sequence 22, Application US/09331930A
; Patent No. 6436670

; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97

```
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-331-930A-22

Alignment Scores:
Pred. No.: 1.15e-36 Length: 73
Score: 331.00 Matches: 59
Percent Similarity: 89.0% Conservative: 6
Best Local Similarity: 80.8% Mismatches: 8
Query Match: 49.8% Indels: 0
Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-22 (1-73)

QY 29 ATGATTGAGTGGTTTGCACGACCGCTCTAGGAAGAAAGTCCGCTTAAGTGCACACC 88
Db 1 MetIleGluIleThrValAsnAspArgLeuGlyLysValArgIleLysCysAsnPro 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 SerAspThrIleGlyAspLeuLysLysLeuIleAlaAlaGlnThrGlyThrArgTrpGlu 40
QY 149 AAGATCGTTCTTAAAAAGTGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysIleValLeuLysLysTrpTyThrIleTyLysAspHisIleThrLeuMetAspTyr 60
QY 209 GAAATCCAGATCGGATGAACCTGGAGCTTTATTACCAG 247
Db 61 GluIleHisGlyPheAsnPheGluLeuTyTrpGln 73

RESULT 8
US-09-331-930A-23
; Sequence 23, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Fasiola hepatica
US-09-331-930A-23

Alignment Scores:
Pred. No.: 1.7e-30 Length: 66
Score: 286.00 Matches: 54
Percent Similarity: 89.4% Conservative: 5
Best Local Similarity: 81.8% Mismatches: 7
Query Match: 43.0% Indels: 0
Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-23 (1-66)

QY 50 GACCGTCTAGGAAGAAGTCCGCTTAAGTGCACACCGATGACACCATCGGGGACTTG 109
Db 1 AspArgLeuGlyLysValArgValLysCysAsnProThrAspLysValGlyAspLeu 20
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QY 110 AAAAACTGATAGCGGCCCAAACTGGCACTCGTTGGAATAAGATCGTTCTTAAAGTGG 169
Db 21 LysLysLeuIleAlaAlaGlnThrGlyThrAlaProGluArgIleValLeuLysLysTrp 40
QY 170 TACACGATTTTAAAGGACCATGTATCTCTGGGAGATTATGAAATCCACGATGGATGAAC 229
Db 41 TyrThrIleTyLysAspHisValThrLeuArgAspTyTrpGluIleAsnAspGlyMetAsn 60
QY 230 CTGGAGCTTTATTACCAG 247
Db 61 LeuGluLeuTyTrpGln 66

RESULT 9
US-09-248-796A-16302
; Sequence 16302, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16302
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16302

Alignment Scores:
Pred. No.: 8.5e-26 Length: 75
Score: 252.00 Matches: 44
Percent Similarity: 77.8% Conservative: 12
Best Local Similarity: 61.1% Mismatches: 16
Query Match: 37.9% Indels: 0
Gaps: 0

US-10-067-832D-1 (1-370) x US-09-248-796A-16302 (1-75)

QY 29 ATGATTGAGTGGTTTGCACGACCGCTCTAGGAAGAAAGTCCGCTTAAGTGCACACC 88
Db 3 MetIleGluIleGlnAlaAsnAspArgLeuGlyLysLysLysLeuLysCysLeuGlu 22
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 23 ThrAspThrIleGlyAspValLysLysIleLeuGlyLeuGlnIleGlyThrProLeuGlu 42
QY 149 AAGATCGTTCTTAAAAAGTGTACACGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db 43 LysIleIleLeuLysLysGlyTyTrpGlnValTyLysAspHisIleThrLeuAspAspTyr 62
QY 209 GAAATCCAGATCGGATGAACCTGGAGCTTTATTACC 244
Db 63 GluIleHisAspGlyPheAsnPheGluLeuTyTrp 74

RESULT 10
US-09-331-930A-16
; Sequence 16, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-09-331-930A-16

Alignment Scores:
Pred. No.: 2,61e-16 Length: 33
Score: 182.00 Matches: 33
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 27.4% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-16 (1-33)

Qy 149 AAGATCGTCTTAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGAGATTAT 208
Db 1 LysileValLeuLysIstIrtYrThrIlePhelysAspHisValSerLeuGlyAspTyr 20
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTACCAG 247
Db 21 GluileHisaspGlyMetAsnLeuGluLeuTyrTrGln 33

RESULT 11
US-09-331-930A-18
; Sequence 18, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-09-331-930A-18

Alignment Scores:
Pred. No.: 2,61e-16 Length: 33
Score: 182.00 Matches: 33
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 27.4% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-18 (1-33)

Qy 149 AAGATCGTCTTAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGAGATTAT 208
Db 1 LysileValLeuLysIstIrtYrThrIlePhelysAspHisValSerLeuGlyAspTyr 20
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTACCAG 247
Db 21 GluileHisaspGlyMetAsnLeuGluLeuTyrTrGln 33
```

```
RESULT 12
US-09-331-930A-14
; Sequence 14, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: variable amino acid
US-09-331-930A-14

Alignment Scores:
Pred. No.: 1,07e-13 Length: 33
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 24.5% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-1 (1-370) x US-09-331-930A-14 (1-33)

Qy 29 ATGATTGAGTGTGTTTCAACGACCGTCTAGGAAGAAAGTCCGCTTAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysVal***ValLysCysAsnThr 20
Qy 89 GATGACACCATCGGGGACTTGAAGAAACTGATAGCGGCC 127
Db 21 AspAspThrileGlyAspLeuLysLeuLeuLeuLeuLeu 33

RESULT 13
US-09-331-930A-27
; Sequence 27, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-331-930A-27
```

Alignment Scores:			
Pred. No.:	0.0354	Length:	60
Score:	80.00	Matches:	19
Percent Similarity:	58.3%	Conservative:	16
Best Local Similarity:	31.7%	Mismatches:	25
Query Match:	12.0%	Indels:	0
DB:	2	Gaps:	0
US-10-067-832D-1 (1-370) x US-09-331-930A-27 (1-60)			
QY	59	GGAAAGAAAGTCGCGTAAAGTCGAACACCGATGACACCATCGGGGACTTGAAGAACTG	118
Db	1	GlyysThrIlelleLeuGlulValgluSerAspThrIleAlaasnVallyysGlulys	20
QY	119	ATACGGGCCCAAACTGGGCACCTCGTTGGGAATAAGATCGTTCTTAAAAAGTGGTACACGATT	178
Db	21	IleGlnVallyysGlulGlylleYasProAspGlnMetLeullePhePheGlyGlnGln	40
QY	179	TTTAAGGACCATGATCTCTCGGAGATTATGAATCCACGATGGGATGAACCTGGAGCTT	238
Db	41	LeuGlulAspGlyValThrLeuGlyAspTyraAspIleHisLysLysSerThrLeuTyrlu	60
RESULT 14			
US-09-583-110-4036			
; Sequence 4036, Application US/09583110			
; Patent No. 6699703			
; GENERAL INFORMATION:			
; APPLICANT: Lynn Doucette-Stamm et al.			
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus			
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics			
; FILE REFERENCE: PATH00-07A			
; CURRENT APPLICATION NUMBER: US/09/583,110			
; CURRENT FILING DATE: 2000-05-26			
; PRIOR APPLICATION NUMBER: US 09/107,433			
; PRIOR FILING DATE: 1998-06-30			
; PRIOR APPLICATION NUMBER: US 60/085,131			
; PRIOR FILING DATE: 1998-05-12			
; PRIOR APPLICATION NUMBER: US 60/051,553			
; PRIOR FILING DATE: 1997-07-02			
; NUMBER OF SEQ ID NOS: 5322			
; SEQ ID NO 4036			
; LENGTH: 1078			
; TYPE: PRT			
; ORGANISM: Streptococcus pneumoniae			
US-09-583-110-4036			
Alignment Scores:			
Pred. No.:	0.869	Length:	1078
Score:	73.50	Matches:	22
Percent Similarity:	46.3%	Conservative:	9
Best Local Similarity:	32.8%	Mismatches:	27
Query Match:	11.1%	Indels:	9
DB:	2	Gaps:	3
US-10-067-832D-1 (1-370) x US-09-583-110-4036 (1-1078)			
QY	65	AAAGTCGCGTAAAGTCGAACACCGATGACACCATCGGGGACTTGAAGAACTGATAGCG	124
Db	140	LysleuargPheLysIleLysThrAspAsnValGlylleAlaLysValArgIlelle	159
QY	125	GCCCAAACTGGC-----ACTGGTTGGGAATAAGATCGTT-----CTTAAAAAG	166
Db	160	GlulSerGlyLysAspLysArgLeuTrpAsnSerAlaThrSerGlyThrLysAsp	179
QY	167	TGGTACAGATTTTAAAGGACCATGATCTCTCGGAGATTATGAATCCACATCGGGATG	226
Db	180	TrpGlnThrIleGluAlaAspTyraSerProThrLeuAspVal-----AspLysIle	196
QY	227	AACCTGGAGCTTTATTACCAG	247
Db	197	LysLeuGluLeuPheTyrglu	203
RESULT 15			

```

US-09-107-433-4843
; Sequence 4843, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 4843:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1080
; SEQUENCE DESCRIPTION: SEQ ID NO: 4843:
US-09-107-433-4843

Alignment Scores:
Pred. No.: 0.87 Length: 1080
Score: 73.50 Matches: 22
Percent Similarity: 46.3% Conservative: 9
Best Local Similarity: 32.8% Mismatches: 27
Query Match: 11.1% Indels: 9
DB: 2 Gaps: 3

US-10-067-832D-1 (1-370) x US-09-107-433-4843 (1-1080)
QY 65 AAAGTCGCGTTAGTCAACACCGATCACACCATCGGGAGCTTCAAGAAACTGATAGCG 124
Db 142 LysLeuAargPheLysIleLysThrAspAsnLysValGlyIleAlaLysValargIleIle 161
QY 125 GCCCAACTGGC-----ACTCGTTGGAAATAGATCGTT-----CTTAAAGAG 166
Db 162 GluGluSerGlyLysAspLysArgLeuTrpAsnSerAlaThrThr-SerGlyThrLysAsp 181
QY 167 TGGTACACGATTTTAAAGCACCATGATCTCTGGGAGATTATGAATCCACCATGGGATG 226
Db 182 TrpGlnThrIleGluAlaAspTy-SerProThrLeuAspVal-----AspLysIle 198

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RESULT 15

Qy 227 AACCTGGAGCTTATTACCAG 247
Db 199 LysLeuGluLeuPheTyrGlu 205

Search completed: April 7, 2006, 23:49:33
Job time : 41.1949 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:48:08 / Search time 26.8877 Seconds
(without alignments)
1149.944 Million cell updates/sec

Title: US-10-067-832D-1
Perfect score: 665
Sequence: 1 gtcccgagattaccagctc.....tttgatgctgcacaaaaaaa 370

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Pgapop 6.0 , Pgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications AA.Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPTC=0 -LOOPT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes02p
-USER=US10067832 @CGN 1.1 405 @runat_07042006_175617_9835 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREAU=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	418	62.9	115	4	US-10-264-049-2463
2	394	59.2	73	5	Sequence 2463, Ap
3	394	59.2	73	5	Sequence 2, Appl1
4	394	59.2	73	5	Sequence 15, Appl
5	394	59.2	73	5	Sequence 16, Appl
6	370	55.6	73	5	Sequence 68, Appl
7	366	55.0	68	4	Sequence 19, Appl
8	354	53.2	73	5	Sequence 250542,
9	339	51.0	73	5	Sequence 20, Appl
10	331	49.8	73	6	Sequence 6522, Ap
11	319	48.0	73	4	Sequence 17, Appl
					Sequence 212296,

12	312	46.9	73	4	US-10-437-963-147593
13	312	46.9	73	4	US-10-767-701-46049
14	312	46.9	73	4	US-10-425-115-233843
15	312	46.9	73	4	US-10-425-115-233846
16	312	46.9	73	4	US-10-425-115-233848
17	312	46.9	73	4	US-10-425-115-233849
18	312	46.9	73	4	US-10-425-115-233851
19	312	46.9	73	4	US-10-425-115-233853
20	311	46.8	73	4	US-10-425-115-288480
21	311	46.8	73	4	US-10-425-115-288482
22	311	46.8	73	4	US-10-425-115-288483
23	311	46.8	73	4	US-10-425-115-288486
24	304.5	45.8	74	4	US-10-424-599-207467
25	300	45.1	73	4	US-10-425-115-288481
26	286	43.0	66	5	US-10-067-832D-18
27	285	42.9	73	5	US-10-739-930-8461
28	281	42.3	73	4	US-10-425-115-288479
29	252	37.9	89	4	US-10-083-357-770
30	252	37.9	320	4	US-10-338-411-11
31	252	37.9	320	4	US-10-389-640-11
32	249	37.4	89	4	US-10-425-115-355452
33	248	37.3	73	4	US-10-425-115-290033
34	244	36.7	82	4	US-10-424-599-191611
35	234	35.2	71	4	US-10-424-599-147197
36	194	29.2	110	4	US-10-424-599-213543
37	184	27.7	70	4	US-10-425-115-302525
38	179.5	27.0	79	4	US-10-425-115-269824
39	170	25.6	63	4	US-10-424-599-229016
40	163	24.5	33	5	US-10-067-832D-14
41	160.5	24.1	93	4	US-10-424-599-266457
42	160.5	24.1	112	4	US-10-425-114-47750
43	160.5	24.1	112	4	US-10-425-114-59753
44	158	23.8	112	4	US-10-425-114-62746
45	158	23.8	113	4	US-10-425-114-61768

ALIGNMENTS

RESULT 1
US-10-264-049-2463
; Sequence 2463, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAl33p1
; CURRENT APPLICATION NUMBER: US/10264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn ver. 3.1
; SEQ ID NO 2463
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2463

Alignment Scores:
Pred. No.: 8.74e-44 Length: 115
Score: 418.00 Matches: 78
Percent Similarity: 96.3% Conservative: 1
Best Local Similarity: 95.1% Mismatches: 3
Query Match: 62.9% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-264-049-2463 (1-115)

QY 2 TTCACGAGATTACGCTCCAGCCACATCATTTAGGTGTTTCACACGACCGCTTAGGA 61
||||:|
Db 34 PheGluAlaIleArgAlaProIleGluValValCysAsnArgPArgLeuGly 53
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QY 62 AAGAAAGTCCGCTTAAGTCAACACCGATGACACCATCGGGACTTGAAGAACTGATA 121
Db |||||||
54 LysLysValArgValLysCysAsnThrAspAspThrIleGlyAspLeuLysLeuLeu 73
QY 122 GCGGCCCAAACTGGCACTCGTTGGAATAAGATCGTTCTTAAAGTGTGATACACGATTTT 181
Db |||||||
74 AlaAlaGlnThrGlyThrArgTrpAsnLysIleValLeuLysLysTrpThrIlePhe 93
QY 182 AAGGACCATATCTCTGGGAGATTATGAATCCACGATCGGATGAACCTGGAGCTTTAT 241
Db |||||||
94 LysAspHisValSerLeuGlyAspTrpGluIleHisAspGlyMetAsnLeuGluLeuTyr 113
QY 242 TACCAG 247
Db |||||||
114 TyrGln 115

RESULT 2

US-10-067-832D-2
; Sequence 2, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-10-067-832D-2

Alignment Scores:
Pred. No.: 8.76e-41 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-067-832D-2 (1-73)

QY 29 ATGATTGAGTGGTTTTCACACGCGCTAGGAAGAAAGTCGCGTTAAGTCAACACC 88
Db 1 MetIleGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuLeuIleAlaGlnThrGlyThrArgTrpAsn 40
QY 149 AAGATCGTTCTTAAAAAGTGTACACCATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db |||||||
41 LysIleValLeuLysLysTrpThrIlePheLysAspHisValSerLeuGlyAspTyr 60
QY 209 GAAATCCACGATGGAGTGAACCTGGAGCTTTATTACCAG 247
Db |||||||
61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTrpGln 73

RESULT 3

US-10-067-832D-15
; Sequence 15, Application US/10067832D

; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-832D-15

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Pred. No.: 8.76e-41 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-067-832D-15 (1-73)

QY 29 ATGATTGAGTGGTTTTCACACGCGCTAGGAAGAAAGTCGCGTTAAGTCAACACC 88
Db 1 MetIleGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
QY 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db |||||||
21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40
QY 149 AAGATCGTTCTTAAAAAGTGTACACCATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db |||||||
41 LysIleValLeuLysLysTrpThrIlePheLysAspHisValSerLeuGlyAspTyr 60
QY 209 GAAATCCACGATGGAGTGAACCTGGAGCTTTATTACCAG 247
Db |||||||
61 GluIleHisAspGlyMetAsnLeuGluLeuTyrTrpGln 73

RESULT 4

US-10-067-832D-16

; Sequence 16, Application US/10067832D
; Publication No. US20050059108A1

; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 73


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;
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-832D-16

Alignment Scores:
Pred. No.: 8,76e-41 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-067-832D-16 (1-73)
Qy 29 ATGATTGAGTGGTTTGCACACCGCTTAGGAAAGAAAGTCCGCTTAAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
Qy 89 GATCACACCATCGGGGACTTGAAGAACTGATAGCGGCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTCGGAGATTAT 208
Db 41 LysileValleuLysLysTrpTyThrilePheLysAspHisValSerLeuGlyAspTyr 60
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTACCAG 247
Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73

RESULT 5
US-10-965-898-68
; Sequence 68, Application US/10965898
; Publication No. US20050084936A1
; GENERAL INFORMATION:
; APPLICANT: Leal, Preeti
; Bandman, Olga
; Hillman, Jennifer L.
; Au-Young, Janice
; Tang, Y. Tom
; Yue, Henry
; Shah, Purvi
; Guegler, Karl J.
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/965,898
; FILING DATE: 18-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,403
; FILING DATE: 31-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0455 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 68:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT19
; CLONE: 3245954
; SEQUENCE DESCRIPTION: SEQ ID NO: 68 :
US-10-965-898-68

Alignment Scores:
Pred. No.: 8,76e-41 Length: 73
Score: 394.00 Matches: 73
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.2% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-965-898-68 (1-73)
Qy 29 ATGATTGAGTGGTTTGCACACCGCTTAGGAAAGAAAGTCCGCTTAAGTGCACACC 88
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
Qy 89 GATCACACCATCGGGGACTTGAAGAACTGATAGCGGCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTrpAsn 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTCGGAGATTAT 208
Db 41 LysileValleuLysLysTrpTyThrilePheLysAspHisValSerLeuGlyAspTyr 60
Qy 209 GAAATCCACGATGGATGAACCTGGAGCTTTATTACCAG 247
Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyrTyrGln 73

RESULT 6
US-10-067-832D-19
; Sequence 19, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975200701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-067-832D-19

Alignment Scores:
Pred. No.: 9,87e-38 Length: 73
Score: 370.00 Matches: 67
Percent Similarity: 97.2% Conservative: 3
Best Local Similarity: 93.1% Mismatches: 2
Query Match: 55.6% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-067-832D-19 (1-73)
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QY 29 ATGATTGAGTGGTTTTCACACGCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetilegluValCysAsnAspArgLeuGlyLysValargValLysCysAsnThr 20
QY 89 GATGACACCATCGGGACTTGAAGAAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTTPAsn 40
QY 149 AGATCGTTCTTAAAAAGTGGTACAGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValLeuLysLysTTPyThrIleTyrLysAspHisileThrLeuAlaAspTyr 60
QY 209 GAAATCCACCATGGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluileHisaspGlyMetGlyLeuGluLeuTyrTyr 72
RESULT 7
US-10-424-599-250542
; Sequence 250542, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250542
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6826C.1.pep
US-10-424-599-250542
Alignment Scores:
Pred. No.: 3,13e-37 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 55.0% Indels: 0
Gaps: 4
US-10-067-832D-1 (1-370) x US-10-424-599-250542 (1-68)
QY 29 ATGATTGAGTGGTTTTCACACGCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetilegluValCysAsnAspArgLeuGlyLysValargValLysCysAsnThr 20
QY 89 GATGACACCATCGGGACTTGAAGAAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaGlnThrGlyThrArgTTPAsn 40
QY 149 AGATCGTTCTTAAAAAGTGGTACAGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValLeuLysLysTTPyThrIleTyrLysAspHisileThrLeuAlaAspTyr 60
QY 209 GAAATCCACCATGGGATGAACCTGGAGCTTTATTAC 232
Db 61 GluileHisaspGlyMetAsnLeu 68
RESULT 8
US-10-067-832D-20
; Sequence 20, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
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; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-067-832D-20
Alignment Scores:
Pred. No.: 1.07e-35 Length: 73
Score: 354.00 Matches: 65
Percent Similarity: 93.1% Conservative: 2
Best Local Similarity: 90.3% Mismatches: 5
Query Match: 53.2% Indels: 0
Gaps: 0
US-10-067-832D-1 (1-370) x US-10-067-832D-20 (1-73)
QY 29 ATGATTGAGTGGTTTTCACACGCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetilegluValCysAsnAspArgLeuGlyLysValargValLysCysAsnThr 20
QY 89 GATGACACCATCGGGACTTGAAGAAACTGATAGCGGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaGlnThrGlyThrArgTTPAsn 40
QY 149 AGATCGTTCTTAAAAAGTGGTACAGATTTTAAAGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValLeuLysLysTTPyThrIleTyrLysAspHisileCysLeuGluAspTyr 60
QY 209 GAAATCCACCATGGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluValHisaspGlnThrAsnLeuGluLeuTyrTyr 72
RESULT 9
US-11-097-143-6522
; Sequence 6522, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6522
; LENGTH: 73
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6522

Alignment Scores:
Pred. No.:      8.64e-34      Length:      73
Score:          339.00      Matches:      63
Percent Similarity: 90.4%      Conservative: 3
Best Local Similarity: 86.3%      Mismatches: 7
Query Match:      51.0%      Indels:      0
DB:               6         Gaps:      0

US-10-067-832D-1 (1-370) x US-11-097-143-6522 (1-73)

Qy 29 ATGATTGAGTGGTTTGCACGACCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluileThrValAsnAspArgLeuGlyLysLysValArgValLysCysAsnPro 20
Qy 89 GATCACACCATCGGGGACTTGAAGAACTGATAGCGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 SerAspThrileGlyAspLeuLysLysLeuileAlaAlaGlnThrGlyThrArgTrpGlu 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValleuLysLysTrpTyThrileTyrlsAspHisleThrLeuMetAspTy 60
Qy 209 GAAATCCACGATGGATGAACCTCGAGCTTTATTACCAG 247
Db 61 GluileHisGluGlyPheAsnPheGluLeuTyTrpGln 73

RESULT 11
US-10-424-599-212296
; Sequence 212296, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212296
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33729C.1.pep
US-10-424-599-212296

Alignment Scores:
Pred. No.:      3.02e-31      Length:      73
Score:          319.00      Matches:      59
Percent Similarity: 91.7%      Conservative: 7
Best Local Similarity: 81.9%      Mismatches: 6
Query Match:      48.0%      Indels:      0
DB:               4         Gaps:      0

US-10-067-832D-1 (1-370) x US-10-424-599-212296 (1-73)

Qy 29 ATGATTGAGTGGTTTGCACGACCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValLeuAsnAspArgLeuGlyLysLysValArgValLysCysAsnAsp 20
Qy 89 GATCACACCATCGGGGACTTGAAGAACTGATAGCGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrileGlyAspLeuLysLysLeuileAlaAlaGlnThrGlyThrArgAlaAsp 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileArgileGlnLysTrpTyThrileTyrlsAspHisleThrLeuLysAspTy 60
Qy 209 GAAATCCACGATGGATGAACCTCGAGCTTTATTACC 244
Db 61 GluileHisAspGlyMetGlyLeuGluLeuTyTrp 72

RESULT 12
US-10-437-963-147593
; Sequence 147593, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
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; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6522
; LENGTH: 73
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6522

Alignment Scores:
Pred. No.:      8.64e-34      Length:      73
Score:          339.00      Matches:      63
Percent Similarity: 90.4%      Conservative: 3
Best Local Similarity: 86.3%      Mismatches: 7
Query Match:      51.0%      Indels:      0
DB:               6         Gaps:      0

US-10-067-832D-1 (1-370) x US-11-097-143-6522 (1-73)

Qy 29 ATGATTGAGTGGTTTGCACGACCGTCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluileThrCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnPro 20
Qy 89 GATCACACCATCGGGGACTTGAAGAACTGATAGCGCCCAAACTGGCACTCGTTGGAAT 148
Db 21 AspAspThrileGlyAspLeuLysLysLeuileAlaAlaGlnThrGlyThrLysHisGlu 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATTTTAAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysileValleuLysLysTrpTyThrilePheLysAspProileArgLeuSerAspTy 60
Qy 209 GAAATCCACGATGGATGAACCTCGAGCTTTATTACCAG 247
Db 61 GluileHisAspGlyMetAsnLeuGluLeuTyTrpGln 73

RESULT 10
US-10-067-832D-17
; Sequence 17, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975200701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 17
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-832D-17

Alignment Scores:
Pred. No.:      9e-33      Length:      73
Score:          331.00      Matches:      59
Percent Similarity: 89.0%      Conservative: 6
Best Local Similarity: 80.8%      Mismatches: 8
Query Match:      49.8%      Indels:      0
DB:               5         Gaps:      0

US-10-067-832D-1 (1-370) x US-10-067-832D-17 (1-73)
```

APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147593
LENGTH: 73
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_48107C.1.pep
US-10-437-963-147593

Alignment Scores:
Pred. No.: 2,35e-30 Length: 73
Score: 312.00 Matches: 58
Percent Similarity: 88.9% Conservative: 6
Best Local Similarity: 80.6% Mismatches: 8
Query Match: 46.9% Indels: 0
Gaps: 0
DB:

US-10-067-832D-1 (1-370) x US-10-437-963-147593 (1-73)
Qy 29 ATGATTGAGTGGTTTGCACGACCGCTAGGAAGAAAGTCCGCGTTAAGTGCACACC 88
Db 1 MetileGluValValLeuAenAspArgLeuGlyLysValArgValLysCysAsnGlu 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGCGACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuValAlaAlaGlnThrGlyThrArgProGlu 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATCTTTAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysIleArgIleGlnLysTrpTyrAsnIleTyrLysAspHisIleThrLeuLysAspTyr 60
Qy 209 GAAATCCACGATGGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluIleHisAspGlyMetGlyLeuGluLeuTyrTyr 72

RESULT 13
US-10-767-701-46049
Sequence 46049, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46049
LENGTH: 73
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C594_1.pep
US-10-767-701-46049

Alignment Scores:
Pred. No.: 2,35e-30 Length: 73
Score: 312.00 Matches: 58
Percent Similarity: 88.9% Conservative: 6
Best Local Similarity: 80.6% Mismatches: 8
Query Match: 46.9% Indels: 0
DB:

DB: 4 Gaps: 0
US-10-067-832D-1 (1-370) x US-10-767-701-46049 (1-73)
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Db 1 MetileGluValValLeuAenAspArgLeuGlyLysValArgValLysCysAsnGlu 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGCGACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuValAlaAlaGlnThrGlyThrArgProGlu 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATCTTTAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysIleArgIleGlnLysTrpTyrAsnIleTyrLysAspHisIleThrLeuLysAspTyr 60
Qy 209 GAAATCCACGATGGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluIleHisAspGlyMetGlyLeuGluLeuTyrTyr 72

RESULT 14
US-10-425-115-233843
Sequence 233843, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 233843
LENGTH: 73
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_144858C.1.pep
US-10-425-115-233843

Alignment Scores:
Pred. No.: 2,35e-30 Length: 73
Score: 312.00 Matches: 58
Percent Similarity: 88.9% Conservative: 6
Best Local Similarity: 80.6% Mismatches: 8
Query Match: 46.9% Indels: 0
Gaps: 0
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US-10-067-832D-1 (1-370) x US-10-425-115-233843 (1-73)
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Db 1 MetileGluValValLeuAenAspArgLeuGlyLysValArgValLysCysAsnGlu 20
Qy 89 GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGCGACTCGTTGGAAT 148
Db 21 AspAspThrIleGlyAspLeuLysLeuValAlaAlaGlnThrGlyThrArgProGlu 40
Qy 149 AAGATCGTCTTAAAAAGTGTACACGATCTTTAAGGACCATGTATCTCTGGGAGATTAT 208
Db 41 LysIleArgIleGlnLysTrpTyrAsnIleTyrLysAspHisIleThrLeuLysAspTyr 60
Qy 209 GAAATCCACGATGGGATGAACCTGGAGCTTTATTAC 244
Db 61 GluIleHisAspGlyMetGlyLeuGluLeuTyrTyr 72

RESULT 15
US-10-425-115-233846
Sequence 233846, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233846
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144860C.1.pap
US-10-425-115-233846

Alignment Scores:
Pred. No.: 2,35e-30 Length: 73
Score: 312.00 Matches: 58
Percent Similarity: 88.9% Conservative: 6
Best Local Similarity: 80.6% Mismatches: 8
Query Match: 46.9% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-1 (1-370) x US-10-425-115-233846 (1-73)

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Qy	89	GATGACACCATCGGGGACTTGAAGAACTGATAGCGGCCCAACTGGCACTCGTTGGAAT	148
Db	21	AspAspThrIleGlyAspLeuLysLeuValAlaGlnThrGlyThrArgProGlu	40
Qy	149	AAGATCGTCTTAAAGTGTGTACACGATTTTAAAGACCATGTATCTCTCGGAGATTAT	208
Db	41	LysIleArgIleGlnLysTrpTyrAsnIleTyrLysAspHisIleThrLeuLysAspTyr	60
Qy	209	GAAATCCAGATGGGATCAACCTGGAGCTTTATTAC	244
Db	61	GluIleHisAspGlyMetGlyLeuGluLeuTyrTyr	72

Search completed: April 7, 2006, 23:55:20
Job time : 136.439 secs

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Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:49:48 ; Search time 3.60593 Seconds
(without alignments)
640.114 Million cell updates/sec

Title: US-10-067-832D-1

Perfect score: 665

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Dgapop 6.0 , Dgapext 7.0

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 368322

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-TRNS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pcet -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs0502p
-USER=US10067832 @CGN 1 1 34 @runat_07042006_175620_9893 -NCPU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Published Applications AA New:*
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4: /SID55/ptodata/1/pubpaa/ECT_NEW PUB.pap.*
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6: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pap.*
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8: /SID55/ptodata/1/pubpaa/US60 NEW PUB.pap.*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	72.5	10.9	860	7 US-11-100-356-6
2	72.5	10.9	867	7 US-11-100-356-3
3	69.5	10.5	135	5 US-09-978-360A-460
4	67.5	10.2	869	7 US-11-100-356-4
5	66.5	10.0	315	7 US-11-096-568A-33836
6	66.5	10.0	332	7 US-11-096-568A-33835
7	66.5	10.0	391	7 US-11-096-568A-33834
8	66	9.9	495	7 US-11-182-016-31
9	65.5	9.8	312	6 US-10-793-626-3104

C 10	65.5	9.8	371	7 US-11-087-099-6646	Sequence 6646, Ap
11	65.5	9.8	650	7 US-11-119-249-7	Sequence 7, Appli
12	65	9.8	654	6 US-10-510-947-6	Sequence 6, Appli
C 13	64.5	9.7	501	7 US-11-172-740-441	Sequence 441, App
C 14	64.5	9.7	668	7 US-11-096-568A-31245	Sequence 31245, A
C 15	64.5	9.7	690	7 US-11-096-568A-31244	Sequence 31244, A
C 16	64.5	9.7	882	7 US-11-096-568A-31243	Sequence 31243, A
C 17	63.5	9.5	258	7 US-11-058-924-6	Sequence 6, Appli
C 18	63	9.5	239	6 US-10-957-569-54	Sequence 54, Appl
C 19	63	9.5	239	7 US-11-097-589-53	Sequence 53, Appl
C 20	62.5	9.4	137	5 US-09-978-360A-765	Sequence 765, App
C 21	62.5	9.4	310	7 US-11-087-099-11274	Sequence 11274, A
C 22	62.5	9.4	360	7 US-11-087-099-11236	Sequence 11236, A
C 23	62.5	9.4	412	6 US-10-485-517-204	Sequence 204, App
C 24	62.5	9.4	463	7 US-11-087-099-9184	Sequence 9184, Ap
C 25	61.5	9.2	377	7 US-11-024-959-350	Sequence 350, App
C 26	61.5	9.2	565	6 US-10-506-454-698	Sequence 698, App
C 27	61	9.2	150	7 US-11-096-568A-26888	Sequence 26888, A
C 28	61	9.2	150	7 US-11-096-568A-26896	Sequence 26896, A
C 29	61	9.2	175	7 US-11-096-568A-26895	Sequence 26895, A
C 30	61	9.2	177	7 US-11-096-568A-26887	Sequence 26887, A
C 31	61	9.2	463	7 US-11-072-512-3058	Sequence 3058, Ap
C 32	60.5	9.1	392	6 US-10-498-691A-7	Sequence 7, Appli
C 33	60.5	9.1	403	7 US-11-096-568A-32637	Sequence 32637, A
C 34	60.5	9.1	426	7 US-11-096-568A-32636	Sequence 32636, A
C 35	60.5	9.1	566	6 US-10-203-486-13	Sequence 13, Appl
C 36	60.5	9.1	566	7 US-11-096-568A-32635	Sequence 32635, A
C 37	60.5	9.1	1273	7 US-11-181-330-8	Sequence 8, Appli
C 38	60	9.0	150	7 US-11-172-740-146	Sequence 146, App
C 39	60	9.0	513	7 US-11-098-686-10835	Sequence 10835, A
C 40	59.5	8.9	1018	7 US-11-096-568A-34025	Sequence 34025, A
C 41	59.5	8.9	1045	7 US-11-096-568A-34024	Sequence 34024, A
C 42	59.5	8.9	1111	7 US-11-142-700-26	Sequence 26, Appl
C 43	59.5	8.9	1111	7 US-11-096-568A-34023	Sequence 34023, A
C 44	59	8.9	523	6 US-10-467-657-5392	Sequence 5392, Ap
C 45	58.5	8.8	371	7 US-11-087-099-5960	Sequence 5960, Ap

ALIGNMENTS

RESULT 1
US-11-100-356-6
; Sequence 6, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-11-100-356-6

Alignment Scores:
Pred. No.: 1.41
Score: 72.50
Percent Similarity: 41.1%
Best Local Similarity: 31.0%
Query Match: 10.9%
DB: 7
Length: 860
Matches: 40
Conservative: 13
Mismatches: 34
Indels: 42
Gaps: 10

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US-10-067-832D-1 (1-370) x US-11-100-356-6 (1-860)
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Db 294 ValGluileAenCysThrArgProAsnAsnAsnThrArgLysSerValArgIleGlyPro 313
QY 83 AAC-----ACCGATGACACCATCGGGACCTTGAAGAACTGATAGCGGCC 127
Db 314 GlyGlnAlaPheTyrAlaThrAsnAspIleIleGlyAsnIleArgGlnAlaHisCysAsn 333
QY 128 CAACACTGGCACTCGTTGGAATAAGATC-----GTTCTTAAAGATGCTGATC----- 172
Db 334 IleSerThrAspArgTrpAsnLysThrLeuGlnGlnValMetLysLysLeuGlnGluHis 353
QY 173 -----ACGATT-----TTTAAGGACCATGTATCTCTGGGAGATTATGAAATCCAC 217
Db 354 PheProAsnLysThrIleLysPheLysProHisAlaGly---GlyAspLeuGluile-Th 372
QY 218 GATGGGATGAACCTGGAGCTTTATTACCAGTAGAGGGGAATTCCTCCACCTTGCCCAACC 277
Db 372 rMet-----HisSerPhe---AsnCysArgGlyGluPhePheTyr----- 384
QY 278 TTGCTTTCTCTCCCGCTCAATTAACACACTGTTGTAGATGCTCATTTTAA----- 329
Db 385 -----CysAsnThrSerAsnLeuPheAsnSe 393
QY 330 -ACAATTCACATGAATAAACTTT 353
Db 393 rThrTyrHisAsnAnglyThrTyr 401
RESULT 2
US-11-100-356-3
; Sequence 3, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; PRIOR FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TV1.8_2
US-11-100-356-3
Alignment Scores:
Pred. No.: 1.41 Length: 867
Score: 72.50 Matches: 40
Percent Similarity: 41.3% Conservative: 12
Best Local Similarity: 31.7% Mismatches: 32
Query Match: 10.9% Indels: 42
DB: 7 Gaps: 10
US-10-067-832D-1 (1-370) x US-11-100-356-3 (1-867)
QY 32 ATTGAGTGGTTTGC-----AACGACCGTCTAGGAAGAAAGTCCGCTTAAGTGC 82
Db 299 ValGluileAenCysThrArgProAsnAsnAsnThrArgLysSerValArgIleGlyPro 318
QY 83 AAC-----ACCGATGACACCATCGGGACCTTGAAGAACTGATAGCGGCC 127
Db 319 GlyGlnAlaPheTyrAlaThrAsnAspValIleGlyAsnIleArgGlnAlaHisCysAsn 338
QY 128 CAAACTGGCACTCGTTGGAATAAGATC-----GTTCTTAAAGATGCTG----- 169
Db 339 IleSerThrAspArgTrpAsnLysThrLeuGlnGlnValMetLysLysLeuGlyGluHis 358
QY 170 -----TACACGATT-----TTTAAGGACCATGTATCTCTGGGAGATTATGAAATCCAC 217
Db 359 PheProAsnLysThrIleGlnPheLysProHisAlaGly---GlyAspLeuGluile-Th 377
QY 218 GATGGGATGAACCTGGAGCTTTATTACCAGTAGAGGGGAATTCCTCCACCTTGCCCAACC 277
Db 377 rMet-----HisSerPhe---AsnCysArgGlyGluPhePheTyr----- 389
QY 278 TTGCTTTCTCTCCCGCTCAATTAACACACTGTTGTAGATGCTCATTTTAA----- 329
Db 390 -----CysAsnThrSerAsnLeuPheAsnSe 398
QY 330 -ACAATTCACATGAAT 344
Db 398 rThrTyrHisSerAsn 403
RESULT 3
US-09-978-360A-460
; Sequence 460, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 460
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -25..-1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39)_
; OTHER INFORMATION: unknown
US-09-978-360A-460
Alignment Scores:
Pred. No.: 2.42 Length: 135
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```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33835
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(332)
; OTHER INFORMATION: Ceres Seq. ID no. 13604300
US-11-096-568A-33835

Alignment Scores:
Pred. No.: 6.45 Length: 332
Score: 66.50 Matches: 23
Percent Similarity: 47.6% Conservative: 17
Best Local Similarity: 27.4% Mismatches: 27
Query Match: 10.0% Indels: 17
DB: 7 Gaps: 5

US-10-067-832D-1 (1-370) x US-11-096-568A-33835 (1-332)
QY 235 CTCAGGTTTCATCCCATCGTGGATTTCATAATCTCCAGAGATACATGGTCTTAAAAAT 176
DB 33 IleArgValHisProArgMetMetPheTyAsnValGluLys-----IleLeuGluPro 50
QY 175 CGTGATACACTTTTAAAGAACGATCTTATTCCAAACGAGTGCCAGTTTGGCCGCTATCAG 116
DB 51 LysLeuArgPhePheLys---AspIleGlyPheThrGlySerGlyLeuGlyLys----- 67
QY 115 TTCTTCAAGTCCCGAGTGTGTCATCGGTGGTGCACCTT-----AAC 74
DB 68 PheValSerGlnAsnSerSerValValGlyValSerLeuValLysLeuLysLeuProThr 87
QY 73 GCGGACTTCTTCTTCTAGACGGTGGTTCGAAACAC-----CTCAAT 32
DB 88 ValGluLeuLysSerIleValAlaProLysHisGluAspLeuProValIleLeuSer 107
QY 31 CATTTGGCTGG 20
DB 108 ArgCysGlyTrp 111

RESULT 7
US-11-096-568A-33834
; Sequence 33834, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33834
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(391)
; OTHER INFORMATION: Ceres Seq. ID no. 13604299
US-11-096-568A-33834

Alignment Scores:
Pred. No.: 6.62 Length: 391
Score: 66.50 Matches: 23
Percent Similarity: 47.6% Conservative: 17
Best Local Similarity: 27.4% Mismatches: 27
Query Match: 10.0% Indels: 17
```

```
DB: 7 Gaps: 5
US-10-067-832D-1 (1-370) x US-11-096-568A-33834 (1-391)
QY 235 CTCAGGTTTCATCCCATCGTGGATTTCATAATCTCCAGAGATACATGGTCTTAAAAAT 176
DB 92 IleArgValHisProArgMetMetPheTyAsnValGluLys-----IleLeuGluPro 109
QY 175 CGTGATACACTTTTAAAGAACGATCTTATTCCAAACGAGTGCCAGTTTGGCCGCTATCAG 116
DB 110 LysLeuArgPhePheLys---AspIleGlyPheThrGlySerGlyLeuGlyLys----- 126
QY 115 TTCTTCAAGTCCCGAGTGTGTCATCGGTGGTGCACCTT-----AAC 74
DB 127 PheValSerGlnAsnSerSerValValGlyValSerLeuValLysLeuLysLeuProThr 146
QY 73 GCGGACTTCTTCTTCTAGACGGTGGTTCGAAACAC-----CTCAAT 32
DB 147 ValGluLeuLysSerIleValAlaProLysHisGluAspLeuProValIleLeuSer 166
QY 31 CATTTGGCTGG 20
DB 167 ArgCysGlyTrp 170

RESULT 8
US-11-182-016-31
; Sequence 31, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-31

Alignment Scores:
Pred. No.: 7.91 Length: 495
Score: 66.00 Matches: 30
Percent Similarity: 28.8% Conservative: 6
Best Local Similarity: 24.0% Mismatches: 37
Query Match: 9.9% Indels: 52
DB: 7 Gaps: 7

US-10-067-832D-1 (1-370) x US-11-182-016-31 (1-495)
QY 299 GAGCCATGGAGAGAAAGCAAGTTGGGCAAGTGGAGGAATTCCTCTACTGGTAAT 240
DB 361 LysProTrpPro-----ProSerProCysThr 369
QY 239 AAAGCTCCAGTTTCA-----TCCCAT----- 219
DB 370 GlnAlaProHisProProArgProValArgTrpSerHisGlyProProSerGlySerTrp 389
QY 218 -----CGTGGATTTCATAATCTCCAGAGATACAT----- 189
DB 390 ProTrpCysArgGlyTrpHisArgLeuProSerAlaHisArgSerArgProArgLeuSer 409
QY 188 -----GGTCCCTTAAAAATCGGTACCACCTTTTAA 159
DB 410 SerGlyGlnIleTrpAlaValGlnSerTrpGlyPro---SerLeuCysArg----- 425
QY 158 GAACGATCTTATTCCAAACGAGTGCCAGTTTGGCCGCTATCAGTTTCT----- 111
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Db 426 ArgArgThrSerProSerArgCysAlaProProProSerProGlyHisProProLeu 445
Qy 110 TCAAGTCCCGATGGTGCATGGGTGGCTAAACCGGACTTCTTCTTAGACGGT 51
Db 446 CysGlnProArgGlyCysHisCysCysLeuHisArgGluProSerArgSerGly 465
Qy 50 CGTTGCAAAACCACT 36
Db 466 ThrSerArgProPro 470

RESULT 9
US-10-793-626-3104
; Sequence 3104, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3104
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3104

Alignment Scores:
Pred. No.: 8.45 Length: 312
Score: 65.50 Matches: 26
Percent Similarity: 37.5% Conservative: 22
Best Local Similarity: 20.3% Mismatches: 33
Query Match: 9.8% Indels: 47
DB: 6 Gaps: 5

US-10-067-832D-1 (1-370) x US-10-793-626-3104 (1-312)
Qy 334 ATTGTTAAAAAT-----GAGCATCTACAAAGTGTAAATAGAGCCAT----- 293
Db 153 IleVallysGlyTyrPheAlaAspGlnLeuGlnGlnTyrPheLeuAlaHisGlyValSer 172
Qy 292 -----GGGAGAGGNAAGCAAGGTGG 272
Db 173 SerGlyllelleAspLeuGlyGlyAsnValLeuThrIleGlyArgGlnProGluThrLeu 192
Qy 271 GCAAGGTGG-----AGCAATTC-----CCTCTACTCGTA 242
Db 193 GlulysTrpHisValGlyValArgAsnProPheHisAspThrLeuProLeuValThr 212
Qy 241 ATAAAGTCCAGGTTCATCCCATCGTGATTTCAATATCTCCAGAGATACATGGTCTT 182
Db 213 LeuSerValGluHisGlnSerValValThrSerGlyIleTyrGluArgTyrPheIleGln 232
Qy 181 AAAAATCGTGTACCACTTTTAAAGACGATCTTATTCACAGCATGCGCAGTTGGCGCG 122
Db 233 GluAsnGlnLeu----- 236
Qy 121 TATCAGTGTCTTCAAGTCCCGATGGTGTGCATCGGTGTGCACCTTAACGGGACTTTCTT 62
Db 237 -----PheHisIleLeuAspSerThrThrGlyTyrProValAspAsnAspIleAla 254
Qy 61 TCCTAGACGGTGGTGGCAACAC 38
Db 255 SerValThrIlelleSerAspHis 262

RESULT 10
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```

US-11-087-099-6646
; Sequence 6646, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6646
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-6646

Alignment Scores:
Pred. No.: 8.69 Length: 371
Score: 65.50 Matches: 28
Percent Similarity: 49.4% Conservative: 16
Best Local Similarity: 31.5% Mismatches: 35
Query Match: 9.8% Indels: 10
DB: 7 Gaps: 4

US-10-067-832D-1 (1-370) x US-11-087-099-6646 (1-371)
Qy 262 AGGAATCCCTCTACTGTGTAATAAAGCTCCAGGTTCCATCCCATCGTGGATTTCAATAATC 203
Db 205 ArgAsnGluProLeuLeuProValPheLeuGluTrpThrProIleValValPheThrLeu 224
Qy 202 TCCAGAGATACATGGTCCCTTAAAAATCGGTACACACTTTTAAAGACGATCTTATTCCA 143
Db 225 SerVal-GlyThrTrp-----LeuTyrSerProTyrSerThrLeuMetAspG1 240
Qy 142 ACGA-----GTGCCAGTTTGGCGCGTATCAGTTTCTTCAAGTCCCGATGGTGTGTCATC 89
Db 240 uAsnHisLeuValLeuPheCysValThrMetSerPheValPheGlyArgMetThrTrpLy 260
Qy 88 GGTGTG-----CACTTAACGGCGACTTTCTTCTTAGACGGTGGTTCGAAACCCATC 35
Db 260 sMetIleLeuAlaHisLeuThrLysGlnProPheProTyrTrpThrValMetLeuTrpPr 280
Qy 34 ATCATTTGGTGGCGAGCTGTATC 10
Db 280 oLeulle---GlyGlyAlaLeulle 287

RESULT 11
US-11-119-249-7
; Sequence 7, Application US/11119249
; Publication No. US20050261190A1
; GENERAL INFORMATION:
; APPLICANT: SK Corp.
; APPLICANT: Ewha Womans University
; APPLICANT: LEE, Kong-Joo
; APPLICANT: KIM, Hee-Jung
; APPLICANT: CHO, Jeong Woo
; APPLICANT: KIM, Eun Joo
; APPLICANT: SONG, Eun Joo
; APPLICANT: MAENG, Cheol Young
; TITLE OF INVENTION: FAS ASSOCIATED FACTOR 1
; FILE REFERENCE: 12120-02USA
; CURRENT APPLICATION NUMBER: US/11/119,249
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/566,966
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US 60/590,327
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 7
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 23:55:38 ; Search time 190 Seconds
(without alignments)
168.814 Million cell updates/sec

Title: US-10-067-832D-2
Perfect score: 394
Sequence: 1 MIEVVCNDRLGKVRKVCNT.....HVSIGDYEIHDGMNLELYQ 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq.21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	100.0	73	2 AAY08413	Aay08413 P. obesus
2	394	100.0	73	3 AAB36290	Aab36290 Israeli s
3	394	100.0	73	4 AAM39680	Aam39680 Human pol
4	394	100.0	89	4 AAM41466	Aam41466 Human pol
5	394	100.0	115	5 ABP41331	Abp41331 Human ova
6	339	86.0	73	4 ABB59910	Abb59910 Drosophila
7	313	79.4	73	3 AAG41925	Aag41925 Arabidops
8	313	79.4	96	3 AAG41924	Aag41924 Arabidops
9	312	79.2	73	3 AAG40885	Aag40885 Zea mays
10	300	76.1	73	3 AAG27281	Aag27281 Zea mays
11	285	72.3	73	8 ADT58384	Adt58384 Plant pol
12	252	64.0	89	5 ADH32312	Adh32312 Novel yea
13	252	64.0	320	6 ABR83620	Abr83620 HUB1-GFP
14	163	41.4	33	2 AAY08414	Aay08414 Human bea
15	163	41.4	33	8 ADR43346	Adr43346 Human bea
16	147.5	37.4	32	3 AAB36291	Aab36291 Human bea
17	138	35.0	27	4 AAM21187	Aam21187 Peptide #
18	138	35.0	27	4 ABB34508	Abb34508 Peptide #
19	138	35.0	27	4 AAM37402	Aam37402 Peptide #
20	138	35.0	27	4 ABB26468	Abb26468 Protein #
21	138	35.0	27	4 AAM77251	Aam77251 Human bon
22	138	35.0	27	4 AAM64443	Aam64443 Human bra
23	138	35.0	27	5 ABG46267	Abg46267 Human pep
24	137	34.8	40	9 ADV95411	Adv95411 Yeast ubi

25	133	33.8	40	9 ADV95410	Adv95410 Yeast ubi
26	120	30.5	32	9 ADV95409	Adv95409 Yeast ubi
27	115	29.2	32	9 ADV95412	Adv95412 Yeast ubi
28	85.5	21.7	857	9 ADX39713	Adx39713 HIV Env p
29	81	20.6	638	9 ADZ07768	Adz07768 HIV CON-A
30	81	20.6	854	9 ADZ07813	Adz07813 HIV CON-0
31	81	20.6	854	9 ADZ07767	Adz07767 HIV CON-A
32	80.5	20.4	857	9 ADX39712	Adx39712 HIV Env p
33	80	20.3	477	3 AAG38562	Aag38562 Arabidops
34	80	20.3	553	3 AAG38561	Aag38561 Arabidops
35	80	20.3	631	3 AAG38560	Aag38560 Arabidops
36	80	20.3	853	9 ADZ04172	Adz04172 Env prote
37	80	20.3	854	9 ADX39709	Adx39709 HIV Env p
38	76	19.3	493	9 ADM69641	Adm69641 HIV-1 gp1
39	76	19.3	831	9 ADZ07806	Adz07806 HIV CON-F
40	75.5	19.2	876	9 ADX39742	Adx39742 HIV Env p
41	74.5	18.9	509	9 ADM69547	Adm69547 HIV-1 gp1
42	74.5	18.9	630	9 ADZ07780	Adz07780 HIV subty
43	74.5	18.9	854	9 ADZ07779	Adz07779 HIV Env p
44	74.5	18.9	857	9 ADX39691	Adx39691 HIV Env p
45	74.5	18.9	1066	8 ADM92082	Adm92082 S pneumon

ALIGNMENTS

RESULT 1
AAY08413
ID AAY08413 standard; protein; 73 AA.
XX
AC AAY08413;
XX
DT 24-JUL-1999 (first entry)
XX
DE P. obesus beacon protein.
XX
KW Beacon, hypothalamus; obese; lean; agonist; antagonist; treatment;
KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;
KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;
KW medicament; livestock; diagnosis.
XX
OS Psammomys obesus.
XX
PN WO9923217-A1.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98WO-AU000902.
XX
PR 31-OCT-1997; 97AU-00000117.
PR 11-NOV-1997; 97AU-00000323.
PA (ITDI-) INT DIABETES INST.
PA (UYDE-) UNIV DEAKIN.
XX
PI Zimmet PZ, Collier G;
DR WPI; 1999-337484/28.
DR N-PSDB; AAX57359.
XX
PT New gene encoding a beacon protein associated with modulation of obesity,
PT diabetes and metabolic energy levels.
XX
PS Claim 2; Page 50; 85pp; English.
XX
CC This invention describes a novel beacon protein and its encoding nucleic
CC acid which is expressed in larger amounts in hypothalamus tissue of obese
CC animals compared to lean animals. Agonists and antagonists of beacon can
CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,
CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
CC resistance. The beacon protein, itself is used to manufacture medicaments
CC for treatment of obesity, anorexia, energy imbalance or diabetes. The
CC treatment is contemplated for both human and animals, such as those

CC important to the livestock industry. The antibody and polynucleotides are
CC useful in diagnosis of conditions as above
XX
SQ Sequence 73 AA;

Query Match	100.0%	Score	394;	DB	2;	Length	73;
Best Local Similarity	100.0%	Pred. No.	7.5e-42;				
Matches	73;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 MIEVVCNDRLGKKVRVKCNTDDTIGDLKLLAAQTGRWNKIVLKKWTIFKHVSLGDY 60
|||
Db 1 MIEVVCNDRLGKKVRVKCNTDDTIGDLKLLAAQTGRWNKIVLKKWTIFKHVSLGDY 60

Qy 61 EIHGGMNLELYYQ 73
|||
Db 61 EIHGGMNLELYYQ 73

RESULT 2
AAB36290
ID AAB36290 standard; protein; 73 AA.

XX	AAB36290;
AC	XX
XX	23-FEB-2001 (first entry)
DT	XX
XX	Israeli sand rat beacon ligand.
DE	XX
XX	Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes; ligand.
KW	
KW	

XX
OS Peamnomys obesus.
XX
XX WO200064931-A1.
XX
XX
XX
PD 02-NOV-2000.
XX
XX
PF 19-APR-2000; 2000WO-AU000342.
XX
XX 23-APR-1999; 99AU-00009919.
PR
PR 24-MAR-2000; 2000AU-00006454.
PR

PA	(AUTO-) AUTOGEN PTY LTD.
XX	
XX	Collier G, Walder K, Zimmet P;
XX	
XX	WPI: 2000-687311/67.
XX	N-PSDB: AAC81767.
XX	
PT	Ligand of beacon protein useful for treating obesity, anorexia, energy
PT	imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and
PT	insulin resistance.

Claim 3; Fig 1; 67pp; English.

The present invention is related to the isolation of a ligand known as beacon from the Israeli sand rat. Beacon is associated with the regulation of energy balance, and the protein, its coding sequence and analogues can be used in the treatment of diabetes, obesity, anorexia, energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and insulin resistance. In addition, they can be used in agriculture to produce leaner animals

Sequence 73 AA;

Query Match	100.0%	Score 394;	DB 3;	Length 73;
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Gaps 0;				

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Qy	1	M	I	E	V	V	C	N	D	R	L	G	K	K	V	R	V	K	C	N	T	D	D	T	I	G	D	L	K	K	L	I	A	A	Q	T	G	T	R	N	K	I	V	L	K	K	W	T	I	F	K	D	H	V	S	L	G	D	Y	60
Db	1	M	I	E	V	V	C	N	D	R	L	G	K	K	V	R	V	K	C	N	T	D	D	T	I	G	D	L	K	K	L	I	A	A	Q	T	G	T	R	N	K	I	V	L	K	K	W	T	I	F	K	D	H	V	S	L	G	D	Y	60

Qy	61	EIHGNNLELYQ	73
Db	61	EIHGNNLELYQ	73
RESULT	3		
AMM39680			
ID	AMM39680	standard; protein; 73 AA.	
XX	AMM39680;		
XX	AC		
XX	AC		
DT	22-OCT-2001	(first entry)	
XX			
DE	Human polypeptide	SEQ ID NO 2825.	

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; aneuploidy; lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.

XX	26-DEC-2000;	2000NO-US03A263.	
PF			
XX			
PR	23-DEC-1999;	99US-00471275.	
PR	21-JAN-2000;	2000US-00488725.	
PR	20-FUN-2000;	2000US-00552317.	
PR	25-APR-2000;	2000US-00598042.	
PR	13-JUL-2000;	2000US-00620312.	
PR	03-AUG-2000;	2000US-00653450.	
PR	14-SEP-2000;	2000US-00652191.	
PR	29-OCT-2000;	2000US-00693036.	
PR	23-NOV-2000;	2000US-00727344.	
XX			
PA	(HYSE-) HYSEO INC.		

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB: AA158836.

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX
PS Example 4; SEQ ID NO 2825; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with neurotropic, immunosuppressant and cytostatic activity. The polynucleotides and polypeptides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 73 AA;

Query Match 100.0%; Score 394; DB 4; Length 73;

CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 394; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. NO. 9.6e-42;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKCNDDTIGDLKLLIAQTGTRWKNKIVLKKWYTFKDHVSLGDY 60
Db 17 MIEVVCNDRLGKVKVKCNDDTIGDLKLLIAQTGTRWKNKIVLKKWYTFKDHVSLGDY 76
QY 61 EIHDCGNLELYQ 73
Db 77 EIHDCGNLELYQ 89
|||||

RESULT 5
ABP41331
ID ABP41331 standard; protein; 115 AA.
XX
AC ABP41331;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HACNC39, SEQ ID NO:2463.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ54408.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 2463; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX

CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders,
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 394; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDDTIGDLKKLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 60
DB 43 MIEVVCNDRLGKVKVCKNTDDTIGDLKKLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 102
QY 61 EIHGGMNLELYQ 73
DB 103 EIHGGMNLELYQ 115

RESULT 6
ABBS9910
ID ABB59910 standard; protein; 73 AA.
XX ABB59910;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 6522.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
FN WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL04013.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 6522; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 73 AA;

Query Match 86.0%; Score 339; DB 4; Length 73;
Best Local Similarity 86.3%; Pred. No. 6.9e-35;
Matches 63; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVCKNTDDTIGDLKKLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 60
DB 1 MIEVVCNDRLGKVKVCKNPDDTIGDLKKLIAAQTGTKEKIVLKKWYTFKDPRLSDY 60
QY 61 EIHGGMNLELYQ 73
DB 61 EIHGGMNLELYQ 73

RESULT 7
AAG41925
ID AAG41925 standard; protein; 73 AA.
XX AAG41925;
XX
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52222.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0132048P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 06-MAY-1999; 99US-0132487P.

XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 79.4%; Score 313; DB 3; Length 73;
Best Local Similarity 80.6%; Pred. No. 1.4e-31;
Matches 58; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKKLIAAQTGRWNKIVLKKWYTFKDHVSLGDY 60
Db 1 MIEVVLNDRLGKVRKVCNDDDTIGDLKKLVAAQTGTAEKIRIQKWNLYKDHITLKDY 60

Qy 61 EIHGGMNLELY 72
Db 61 EIHGGMLELY 72

RESULT 8
AAG41924
ID AAG41924 standard; protein; 96 AA.
XX
AC AAG41924;
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52221.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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Query Match 79.4%; Score 313; DB 3; Length 96;
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Qy 61 EIHDMNLELYY 72
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
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XX
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Query Match          79.2%; Score 312; DB 3; Length 73;
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Qy 61 EIHGGMNLELYY 72
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RESULT 10
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AC AAG27281;
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DT 17-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 32055.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
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PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151338P.
PR 01-SEP-1999; 99US-0151930P.
PR 01-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 76.1%; Score 300; DB 3; Length 73;
Best Local Similarity 76.4%; Pred. No. 6e-30; Indels 0; Gaps 0;
Matches 55; Conservative 8; Mismatches 9;

QY 1 MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTTRWNKIVLKKWYTFKDHVSLG DY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MIEVVLNDRLGKKVRVKCNEDDTIGDLNKLVAQAQTGTREKIRIQKWNYYKDYITLKDY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 EIHGGMNLELYY 72
    |:||||| |||||
Db 61 EVHDSGMGLELYY 72
    |:||||| |||||

RESULT 11
ADT58384
ID ADT58384 standard; protein; 73 AA.
XX
AC ADT58384;
XX
DT 13-JAN-2005 (first entry)
XX
DE Plant polypeptide, SEQ ID 8461.
XX
KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.
XX
OS Viridiplantae.
XX
PN US2004216190-A1.
XX
PD 28-OCT-2004.
XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.
XX
PI Kovalic DK;
XX
WPI; 2004-757369/74.
XX
PT New recombinant DNA constructs useful in the field of biochemistry and
PT Genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.
XX
PS Claim 2; SEQ ID NO 8461; 14pp; English.
XX
CC The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
```

CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.

CC Sequence 73 AA;

Query Match 72.3%; Score 285; DB 8; Length 73;
Best Local Similarity 76.7%; Pred. No. 4.8e-28;
Matches 56; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

QY 1 MIEVVCDRLGKVKVRKCNDDTTIGDLKGLIAAQTG-TRWNKIVLKKWYTFKDHVSLGD 59
DB 1 MIEVVCDRLGKVKVRKXC-XDDTTIGDLKGLVAAQTGTRPEKIRIQKWNYYIKDHITLKD 59
QY 60 YEIHGGMNLELY 72
DB 60 YEIHGGMNLELY 72

RESULT 12

ID ADH32312
AC ADH32312 standard; protein; 89 AA.

XX ADH32312;

XX 11-MAR-2004 (first entry)

XX Novel yeast smORF572-encoded polypeptide, SEQ ID NO:770.

XX Open reading frame; ORF; identification; in silico; yeast; smORF;
XX small open reading frame; antisense therapy; antibody therapy;
XX drug screening; fungal infection; fungicide; gene therapy; vaccine.

XX Saccharomyces cerevisiae.

XX WO200268693-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US005677.

XX 27-FEB-2001; 2001US-0271406P.

XX 29-NOV-2001; 2001US-0333726P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Zeng Q, Kessler M, Cottarel G;

XX WPI; 2002-707018/76.

XX N-PSDB; ADH31639.

XX Identifying open reading frames (ORFs) in a genome of an organism by-
XX comparing genomic sequences to one or more genomic libraries containing
XX ORFs, useful for diagnosing, preventing and/or treating fungal
XX infections.

XX Claim 38; SEQ ID NO 770; 160pp; English.

XX The invention relates to a method of identifying open reading frames

CC (ORFs) in a genome of an organism. The method comprises: collecting a
CC genomic sequence of a first organism; comparing the genomic sequence of
CC the first organism to one or more other genomic libraries comprising
CC genomes of other organisms containing ORFs; and determining ORFs for the
CC first organism based on the comparison. The invention also relates to
CC smORFs (small open reading frames) from the Saccharomyces cerevisiae
CC genome which encode polypeptides less than 100 amino acids long; vectors
CC and host cells comprising a smORF; polypeptides encoded by the smORFs;
CC antisense compounds targeted to the smORFs and methods for their use in
CC inhibiting smORF expression; a method of identifying an inhibitor of a
CC smORF-encoded protein; an antibody against a smORF-encoded polypeptide;
CC and a composition comprising a smORF or smORF-encoded polypeptide and a
CC carrier. The invention provides a useful in silico method of identifying
CC new coding sequences, including homologues of coding sequences, in yeast
CC and other organisms. The compositions of the invention, and methods of
CC their use or discovery are also useful for diagnosing, preventing and/or
CC treating fungal infections. Sequences ADH32216-ADH32888 represent
CC specifically claimed yeast smORF-encoded polypeptides. Note: The sequence
CC data for this patent is not represented in the printed specification but
CC is based on sequence information supplied to Derwent by the European
CC Patent Office.

SQ Sequence 89 AA;

Query Match 64.0%; Score 252; DB 5; Length 89;
Best Local Similarity 65.3%; Pred. No. 9.3e-24;
Matches 47; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MIEVVCDRLGKVKVRKCNDDTTIGDLKGLIAAQTGTRWNKIVLKKWYTFKDHVSLGDY 60
DB 17 MIEVVCDRLGKVKVRKCLAEEDSVGDFKVLQIGTQPNKIVLQKGGSVLKHISLEDY 76

QY 61 EIHGGMNLELY 72

DB 77 EVHDQTNLELY 88

RESULT 13

ABR83620
ID ABR83620 standard; protein; 320 AA.

XX ABR83620;

XX 16-OCT-2003 (first entry)

XX HUB1-GFP protein sequence SEQ ID NO:11.

XX Protein expression; purification; fusion protein; SUMO; GFP; RUB; HUB;
XX green fluorescent protein; enhancing protein expression level; APG8;
XX AFG12; URM1; ISG15; secretion.

XX Homo sapiens.

XX Asquorea victoria.

XX Synthetic.

XX WO2003057174-A2.

XX 17-JUL-2003.

XX 07-JAN-2003; 2003WO-US000436.

XX 07-JAN-2002; 2002US-0346449P.

XX (LIFE-) LIFESENSORS INC.

XX Butt TR, Weeks SD, Tran HT, Malakhov MP, Malakhova OA;

XX WPI; 2003-577500/54.

XX N-PSDB; ACF57380.

XX Enhancing protein expression levels in or from a cell comprises operably
XX linking ubiquitin or ubiquitin-like proteins to a nucleic acid encoding a
XX protein to generate a construct encoding a fusion protein for expression

PT in a host cell.
 XX Example 1; Fig 28A-B; 144pp; English.
 XX

CC The present invention describes a method for enhancing expression levels
 CC of a protein in or from a cell. The method comprises: (a) operably
 CC linking a nucleic acid sequence encoding SUMO, RUB, HUB, APG8, APG12,
 CC URM1 or ISG15, to a nucleic acid sequence encoding the protein to a
 CC generate a construct encoding a fusion protein; and (b) introducing the
 CC nucleic acid into a host cell, where the presence of the molecule in the
 CC fusion protein increases the expression level or the secretion of the
 CC protein in the host cell. The method is useful for enhancing protein
 CC expression, and for generating novel amino termini on proteins of
 CC interest for a variety of research, diagnostic and therapeutic
 CC applications. The method of enhancing protein circumvents problems
 CC encountered with previous methods by enhancing the expression of under-
 CC expressed proteins, increasing the solubility of proteins that are
 CC insoluble, protecting the candidate proteins from degradation by
 CC intracellular proteases by fusing ubiquitin-like proteins (UBLs) to their
 CC N-termini, cleaving the fusion protein to efficiently generate authentic
 CC proteins using naturally present enzymes, generating proteins with novel
 CC amino termini, and cleaving all fusion proteins with remarkable
 CC efficiency irrespective of the N-terminal sequence of the fused protein,
 CC using UBL hydrolases. The present sequence represents a HUB1-GFP protein
 CC sequence, which is used in the exemplification of the present invention
 XX
 SQ Sequence 320 AA;

Query Match 64.0%; Score 252; DB 6; Length 320;
 Best Local Similarity 65.3%; Pred. No. 4.7e-23;
 Matches 47; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGRWNKIVLKKWYIFKDHVSLGDY 60
 DB 10 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGRWNKIVLKKWYIFKDHVSLGDY 69
 QY 61 EIHGDMNLELY 72
 DB 70 EVHDQTNLELY 81

RESULT 14
 ID AAY08414
 XX AAY08414 standard; protein; 33 AA.
 AC AAY08414;
 XX
 XX 24-JUL-1999 (first entry)
 XX Human beacon protein.
 DE
 XX Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;
 KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;
 KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;
 KW medicament; livestock; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 15
 FT /label= unknown
 FT /note= "encoded by CNC"
 XX
 XX WO9923217-A1.
 XX
 XX 14-MAY-1999.
 XX
 XX 30-OCT-1998; 98WO-AU000902.
 XX
 XX 31-OCT-1997; 97AU-00000117.
 PR 11-NOV-1997; 97AU-00000123.
 XX
 XX (ITDI-) INT DIABETES INST.
 PA

(UYDE-) UNIV DEAKIN.
 XX
 XX Zimmet PZ, Collier G;
 XX
 DR WPI; 1999-337484/28.
 DR N-PSDB; AAX57370.
 XX
 PT New gene encoding a beacon protein associated with modulation of obesity,
 PT diabetes and metabolic energy levels.
 XX
 PS Claim 2; Page 54; 85pp; English.
 XX
 CC This invention describes a novel beacon protein and its encoding nucleic
 CC acid which is expressed in larger amounts in hypothalamus tissue of obese
 CC animals compared to lean animals. Agonists and antagonists of beacon can
 CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
 CC resistance. The beacon protein, itself is used to manufacture medicaments
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The
 CC treatment is contemplated for both human and animals, such as those
 CC important to the livestock industry. The antibody and polynucleotides are
 CC useful in diagnosis of conditions as above
 XX
 SQ Sequence 33 AA;
 Query Match 41.4%; Score 163; DB 2; Length 33;
 Best Local Similarity 97.0%; Pred. No. 4.9e-13;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAA 33
 DB 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAA 33

RESULT 15
 ID ADR43346
 XX ADR43346 standard; peptide; 33 AA.
 AC ADR43346;
 XX
 XX 04-NOV-2004 (first entry)
 XX Human Beacon protein.
 DE
 XX Beacon; Anorectic; Anabolic; Antidiabetic; Cytostatic; Cardiant;
 KW Antiinflammatory; Immunosuppressive; Antinfertility; Neuroprotective;
 KW Nootropic; CLK; myopathy; obesity; anorexia; diabetes; cancer;
 KW heart disease; inflammation; Alzheimer's; Parkinson's; Pearson Syndrome;
 KW Pyruvate Carboxylase Deficiency; Pyruvate Dehydrogenase Deficiency;
 KW Cancer; Acoustic Neuroma; Acute Lymphocytic Leukemia; Carcinoma;
 KW Leukemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2004069866-A1.
 XX
 XX 19-AUG-2004.
 XX
 XX 10-FEB-2004; 2004WO-AU000147.
 PF
 XX 10-FEB-2003; 2003US-0446191P.
 PR
 XX (AUTO-) AUTOGEN RES PTY LTD.
 PA (UYDE-) UNIV DEAKIN.
 XX
 XX Collier G, Walder K, Kerr-Bayles L;
 PI
 XX WPI; 2004-604412/58.
 DR
 XX New isolated ligands of mammalian or avian Beacon, useful for e.g.
 PT preventing or treating disorders associated with myopathy, obesity,
 PT diabetes, cancer, heart disease, inflammation, or disorders associated
 PT with the immune system.

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Query Match      77.7%; Score 306; DB 2; Length 73;
Best Local Similarity 79.2%; Pred. No. 9.4e-28;
Matches 57; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVRVKCNVTDITGDLKKLIAAQTGRWNKIVLKKWYTFKDHVSLGDY 60
DB 1 MIEVLNDRLGKKVRVKCNVEDITGDLKKLVAAQTGTREKIRIQKNYIKDHIPLKDY 60

QY 61 EIHGGMNLELYY 72
DB 61 EIHGGMGLELYY 72

RESULT 3
T40200
ubiquitin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40200
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21912
A:Accession: T40200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-73 <OLI>
A:Cross-references: UNIPROT:O94650; UNIPARC:UPI000006A678; EMBL:AL049190; PIDN:CAB39137.
A:Experimental source: strain 972h-; cosmid c31E1
C:Genetics:
A:Gene: SPDB:SPBC31E1.03
A:Map position: 2
A:Introns: 6/2; 40/2

Query Match      76.4%; Score 301; DB 2; Length 73;
Best Local Similarity 73.6%; Pred. No. 3.5e-27;
Matches 53; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVRVKCNVTDITGDLKKLIAAQTGRWNKIVLKKWYTFKDHVSLGDY 60
DB 1 MIEVLNDRLGKKVRVKCMPDDTVDGDFKKLVAAQTGTPRRIVLKKWHSVFKDNITLADY 60

QY 61 EIHGGMNLELYY 72
DB 61 EIHGGMNLEMY 72

RESULT 4
S78735
protein YNR032c-a - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999
C:Accession: S78735
R:Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63346
A:Accession: S78735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <POH>
A:Cross-references: UNIPARC:UPI0000168403; EMBL:Z71647; MIPS:YNR032c-a
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 14R

Query Match      64.0%; Score 252; DB 2; Length 73;
Best Local Similarity 65.3%; Pred. No. 1.3e-21;
Matches 47; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKKVRVKCNVTDITGDLKKLIAAQTGRWNKIVLKKWYTFKDHVSLGDY 60
DB 1 MIEVWVNDRLGKKVRVKCLAEDSVGDFKKVLSLQIGTPPNKIVLKGGSVLKDHISLEDY 60
```

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QY 61 EIHGGMNLELYY 72
DB 61 EVHDQTNLELYY 72

RESULT 5
S55243
ubiquitin-like protein 8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
C:Accession: S55243; S61068
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
Genetics 139, 921-939, 1995
A:Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like protein
A:Reference number: S55243; MUID:95229071; PMID:7713442
A:Accession: S55243
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-631 <CAL>
A:Cross-references: UNIPROT:Q39256; UNIPARC:UPI000017A48A; EMBL:L05917
A:Experimental source: ecotype Columbia
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
submitted to the EMBL Data Library, June 1995
A:Reference number: S61068
A:Accession: S61068
A:Molecule type: DNA
A:Residues: 1-341, E', 343-631 <CAN>
A:Cross-references: UNIPARC:UPI00000A3588; EMBL:L05917; NID:g870793; PIDN:AAA68879.1; PII
F:79-154/Domain: ubiquitin homology <UBH1>
F:155-237/Domain: ubiquitin homology <UBH2>
F:238-318/Domain: ubiquitin homology <UBH3>
F:319-392/Domain: ubiquitin homology <UBH4>
F:393-468/Domain: ubiquitin homology <UBH5>
F:469-551/Domain: ubiquitin homology <UBH6>
F:552-627/Domain: ubiquitin homology <UBH8>

Query Match      20.3%; Score 80; DB 2; Length 631;
Best Local Similarity 31.7%; Pred. No. 0.41;
Matches 19; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 11 GKKVRVKCNVTDITGDLKKLIAAQTGRWNKIVLKKWYTFKDHVSLGDIYHIDGMNLEL 70
DB 561 GXTIILEVSSDTIANVKEIQVKGIGKPDQQLIFFGQQLDGVTLGDYDIHKKSTLYL 620

RESULT 6
B95037
hyaluronidase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95037
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95037
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1066 <KUP>
A:Cross-references: UNIPROT:Q54873; UNIPARC:UPI000012D052; GB:AE005672; PIDN:AAK74491.1
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0314

Query Match      18.9%; Score 74.5; DB 2; Length 1066;
Best Local Similarity 34.3%; Pred. No. 3;
Matches 23; Conservative 8; Mismatches 27; Indels 9; Gaps 3;

QY 13 KVRVKCNVTDITGDLKKLIAAQTG---TRWNKIV---LKKWYTFKDHVSLGDIYHIDGM 66
```



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Db      128 KLRFKIKTDNKIGIAKVIIEESGKDKLWNSATTSCTGKDWQTIHEADYSPTLDV---DKI 184
Qy      67 NLELYYQ 73
Db      185 KLELFYE 191

RESULT 7
F97907
hyaluronate lyase (EC 4.2.2.1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: F97907
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Accession: F97907
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1078 <KUR>
A:Cross-references: UNIPROT:Q8CWU3; UNIPARC:UPI000000E4928; GB:AE007317; PIDN:AAK99090.1;
C:Genetics:
A:Gene: hyaA
C:Keywords: carbon-oxygen lyase

Query Match      18.7%; Score 73.5; DB 2; Length 1078;
Best Local Similarity 32.8%; Pred. No. 4;
Matches 22; Conservative 9; Mismatches 27; Indels 9; Gaps 3;

Qy      13 KVRVKCNTDDTIGDLKKLIAAQTG---TRWNKIV---LKKWYTFKDHVSLGSDYIEHDGM 66
Db      140 KLRFKIKTDNKVGIAKVIIEESGKDKLWNSATTSCTGKDWQTIHEADYSPTLDV---DKI 196
Qy      67 NLELYYQ 73
Db      197 KLELFYE 203

RESULT 8
S60529
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-14-13) (frac
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-14-13
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60529
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60529
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <JAN>
A:Cross-references: UNIPROT:Q76172; UNIPARC:UPI0000010385B; EMBL:X72031; NID:G468637; PID
A:Experimental source: isolate CI-14-13
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match      17.9%; Score 70.5; DB 2; Length 299;
Best Local Similarity 27.7%; Pred. No. 2.2;
Matches 23; Conservative 11; Mismatches 20; Indels 29; Gaps 3;

Qy      9 RLGKVRVKCN-----TDDTIGDLKKLIAAQTGTRWNKIV----- 43
Db      20 QLVKPVIRNTRPSNTRKSVIPGPGAFATDDIIGIRQAHNCVSKTEWNETLQOVAT 79

RESULT 9
S60528
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-14-5 and iso
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-14-5; isolate CI-14-21
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60528; S60530
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60528
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <JAN>
A:Cross-references: UNIPROT:Q76171; UNIPROT:Q76173; UNIPARC:UPI0000101A6F; EMBL:X72030;
A:Experimental source: isolate CI-14-5
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <JAN>
A:Cross-references: UNIPARC:UPI0000101A6F; EMBL:X72032; NID:G468639; PIDN:CAA50915.1; P1
A:Experimental source: isolate CI-14-21
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match      17.9%; Score 70.5; DB 2; Length 299;
Best Local Similarity 27.7%; Pred. No. 2.2;
Matches 23; Conservative 11; Mismatches 20; Indels 29; Gaps 3;

Qy      9 RLGKVRVKCN-----TDDTIGDLKKLIAAQTGTRWNKIV----- 43
Db      20 QLVKPVIRNTRPSNTRKSVIPGPGAFATDDIIGIRQAHNCVSKTEWNETLQOVAT 79

RESULT 10
T29404
hypothetical protein C16C8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29404
R:Waterston, R.; Le, T.T.; Gattung, S.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid C16C8.
A:Reference number: Z20617
A:Accession: T29404
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <WAT>
A:Cross-references: UNIPROT:P91057; UNIPARC:UPI000007F11D; EMBL:U80452; PIDN:AAB37860.1;
A:Experimental source: strain Bristol N2; clone C16C8
C:Genetics:
A:Gene: CRSP:C16C8.4
A:Map position: 2
A:Introns: 27/3; 199/1

Query Match      17.5%; Score 69; DB 2; Length 226;
Best Local Similarity 26.5%; Pred. No. 2.4;
Matches 18; Conservative 13; Mismatches 29; Indels 8; Gaps 2;
```

```
QY 10 LGKKVRVKNYDDTIGDLKLLIAAQ-----TGTRWNKIVLKKWYTIFKDHVSLGDDYEHG 65
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 161 LGVSYAFKIHREDTVDFKNDIEHRHDIPQHSWLSFGKR-----LEDHCSIGDYNIQKS 216
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 66 MNLELYYQ 73
: :||| :
Db 217 STITMYFR 224
: :||| :

RESULT 11
mannose-1-phosphate guanylttransferase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70363
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70363
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-831 <AQF>
A:Cross-references: UNIPROT:O66933; UNIPARC:UPI000005641F; GB:AE000704; NID:g2983301; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: mp9

Query Match 17.4%; Score 68.5; DB 2; Length 831;
Best Local Similarity 27.4%; Pred. No. 11;
Matches 23; Conservative 17; Mismatches 21; Indels 23; Gaps 5;

QY 4 VVCND-RLGKKVRVK-----CNTDDTIGDLKLLIAAQTGTRWNKIVLKKWYTIFKDH 54
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 322 VICNDVKIGRKVAKGCVTAEDCEDEVLEFLKDVV-----WPEKIEKGSVVTKNI 375
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 55 VSLGDYE--IHGD-----MNLEL 70
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 376 VCESKWEKGIFGKNVIGRINVEL 399
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
S60545
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-1) (fragme
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-45-1
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60545
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60545
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76190; UNIPARC:UPI0000101898; EMBL:X72047; NID:g468669; PID
A:Experimental source: isolate CI-45-1
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; Glycoprotein; immunodeficiency; polyprotein

Query Match 17.3%; Score 68; DB 2; Length 294;
Best Local Similarity 26.8%; Pred. No. 4.2;
Matches 22; Conservative 11; Mismatches 21; Indels 28; Gaps 3;

QY 9 RLGKKVRVKCN-----TDDTIGDLKLLIAAQTGTRWNKIV----- 43
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 20 QLAKPVKINCTRPNNNTRKSVRIGPGQTFYATGDIIGIRQAHCNVSGTEWNETLQKVA 79
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 54 VVCND-RLGKKVRVK-----CNTDDTIGDLKLLIAAQTGTRWNKIVLKKWYTIFKDH 54
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 322 VICNDVKIGRKVAKGCVTAEDCEDEVLEFLKDVV-----WPEKIEKGSVVTKNI 375
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 55 VSLGDYE--IHGD-----MNLEL 70
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 376 VCESKWEKGIFGKNVIGRINVEL 399
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 13
S60524
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-3) (fragme
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-45-3
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60524
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.; C
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60524
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76168; UNIPARC:UPI000010200C; EMBL:X72027; NID:g468780; PID
A:Experimental source: isolate CI-45-3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; Glycoprotein; immunodeficiency; polyprotein

Query Match 17.3%; Score 68; DB 2; Length 294;
Best Local Similarity 26.8%; Pred. No. 4.2;
Matches 22; Conservative 11; Mismatches 21; Indels 28; Gaps 3;

QY 9 RLGKKVRVKCN-----TDDTIGDLKLLIAAQTGTRWNKIV----- 43
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 20 QLAKPVKINCTRPNNNTRKSVRIGPGQTFYATGDIIGIRQAHCNVSGTEWNETLQKVA 79
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 44 -LKKWY--TIFKDHVSLGDDYEI 62
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 80 QLRKHFNKTIIFASPSGGDVEI 101
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 13
S60524
envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-3) (fragme
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-45-3
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60524
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.; C
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60524
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76168; UNIPARC:UPI000010200C; EMBL:X72027; NID:g468780; PID
A:Experimental source: isolate CI-45-3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; Glycoprotein; immunodeficiency; polyprotein

Query Match 17.3%; Score 68; DB 2; Length 294;
Best Local Similarity 26.8%; Pred. No. 4.2;
Matches 22; Conservative 11; Mismatches 21; Indels 28; Gaps 3;

QY 9 RLGKKVRVKCN-----TDDTIGDLKLLIAAQTGTRWNKIV----- 43
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 20 QLAKPVKINCTRPNNNTRKSVRIGPGQTFYATGDIIGIRQAHCNVSGTEWNETLQKVA 79
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 44 -LKKWY--TIFKDHVSLGDDYEI 62
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 80 QLRKHFNKTIIFASPSGGDVEI 101
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

```
Db      || : | |:|::||| ::|||::|||::|||::|||::
580 DDEVGIQKRLVSCRIGSEWR---FSEWYFFITDHLHYIFEVEAKEVTSTELIF 629
```

REC'D
C97816

aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Rickettsia conorii (strain Malish 7)
C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: G97816
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Sam-
Science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii
A/Reference number: A97700; PMID:21442074; PMID:11557893

Query Match 16.9%: Score 66.5: DB 2: Length 185:

7 NDRLGKKVRVKCNTDDTIGDLKKLIAAOTGTRWN-----KIVLKKWYTI FKDHVSLGDYE 61

62 IHGGMNLE 69

— — — — —

Search completed: April 8, 2006 00:04:11

Job time : 41 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 23:56:33 ; Search time 233 Seconds
(without alignments)
221.045 Million cell updates/sec

Title: US-10-067-832D-2

Perfect score: 394

Sequence: 1 MEVVCNDRLGKKVRVKCNT.....HVSGLDYEIHGNNLELYIQ 73

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	394	100.0	73	1	UBL5_HUMAN	Q9bz11 homo sapien
2	394	100.0	73	1	UBL5_MESAU	Q6egx7 mesocricetu
3	394	100.0	73	1	UBL5_MOUSE	Q9epv8 mus musculu
4	394	100.0	73	1	UBL5_PSAOB	Q791b0 psammomys o
5	394	100.0	73	2	Q5RC10_PONPY	O5rc10 pongo pygma
6	394	100.0	73	2	Q4RSJ3_MACFA	Q4rsj3 macaca fasc
7	368	93.4	73	1	UBL5_BEARE	Q78xf2 brachydanio
8	367	93.1	73	2	Q5HZC1_XENLA	Q5hzc1 xenopus lae
9	354	89.8	73	2	Q4SM16_TETNG	Q4sm16 tetraodon n
10	344	87.3	73	2	Q7QHM2_ANOGA	Q7qhm2 anopheles g
11	339	86.0	73	1	UBL5_DROME	Q9v998 drosophila
12	331	84.0	73	1	UBL5_CAERL	P91302 caenorhabdi
13	331	84.0	73	2	Q617M9_CAERL	Q617m9 caenorhabdi
14	329	83.5	73	2	Q5B857_SCHUA	Q5b857 schistosoma
15	325	82.5	73	2	Q4VAF8_MOUSE	Q4vaf8 mus musculu
16	315	79.9	73	2	Q6K220_ORYSA	Q6k220 oryza sativ
17	313	79.4	73	1	UBL5_ARATH	Q9fgz9 arabidopsis
18	313	79.4	73	2	Q570V8_ARATH	Q570v8 arabidopsis
19	308	78.2	73	2	Q7R8W4_PLAYO	Q7r8w4 plasmodium
20	308	78.2	73	2	Q4YUJ7_PLABE	Q4yuj7 plasmodium
21	306	77.7	73	2	Q9MU11_ARATH	Q9mu11 arabidopsis
22	302	76.6	73	2	H81545_PLAF7	O81545 plasmodium
23	301	76.4	73	1	HUB1_SCHPO	Q94650 schizosacch
24	293	74.4	73	2	Q4M258_THEPA	Q4m258 theileria p
25	291	73.9	76	2	Q4UBE9_THEAN	Q4ube9 theileria p
26	288	73.1	276	2	Q55W54_CRYNE	Q55m54 cryptosoccu
27	288	73.1	276	2	Q5K8L5_CRYNE	O5k8l5 cryptosoccu
28	266	67.5	73	1	HUB1_DBPHA	Q6bup7 debaryomyce
29	263	66.8	70	2	Q6C104_YARLI	O6ci04 yarrowia li
30	250	63.5	47	2	Q5BJ51_RAT	O5bj51 rattus norv
31	248	62.9	73	1	HUB1_YEAST	Q6q546 saccharomyc

32	243	61.7	73	1	HUB1_CANGA	Q6fix7 candida gla
33	238.5	60.5	74	1	HUB1_KLULA	Q6cul2 kluyveromyc
34	238.5	60.5	79	2	Q6CUI1_KLULA	Q6cul1 kluyveromyc
35	235	59.6	73	1	HUB1_ASHGO	Q756x3 ashbya gos
36	231	58.6	87	2	Q540Q3_DICDI	O54q03 dictyocteli
37	214	54.3	79	2	Q509Q3_ENTHI	Q50p03 entanceba h
38	168	42.6	73	2	Q4P9W2_USTWA	Q4p9w2 ustilago ma
39	154.5	39.2	237	2	Q4I016_GIBZE	Q4i016 gibberella
40	141.5	35.9	616	2	Q5BCG2_EMENI	Q5bcg2 aspergillus
41	123.5	31.3	239	2	Q526Z0_MAGGR	Q526z0 magnaporth
42	119.5	30.3	261	2	Q8X065_NEUCR	Q8x065 neurospora
43	113.5	28.8	189	2	Q4WYK6_ASPTU	Q4wyk6 aspergillus
44	94	23.9	219	2	Q6DWES_9HIVI	Q6dwe5 human immun
45	93	23.6	115	2	Q7ZCU2_9HIVI	Q7zcu2 human immun

ALIGNMENTS

RESULT 1
ID UBL5_HUMAN STANDARD; PRT; 73 AA.
AC Q9BZL1;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Ubiqutin-like protein 5.
GN Name=UBL5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=iris.
RX MEDLINE=21100898; PubMed=11161819; DOI=10.1006/geno.2000.6439;
RA Friedman J.S., Koop B.F., Raymond V., Walter M.A.;
RT "Isolation of a ubiquitin-like (UBL5) gene from a screen identifying
RT highly expressed and conserved iris genes.";
RL Genomics 71:252-255(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kainane N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueffin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

RN (4)
RP STRUCTURE BY NMR, AND INTERACTION WITH CLK4.
RX MEDLINE=22709234; PubMed=12824502; DOI=10.1110/ps.0382803;
RA McNally T., Huang Q., Janis R.S., Liu Z., Olejniczak E.T.,
RT Reilly R.M.;
RA "Structural analysis of UBL5, a novel ubiquitin-like modifier.";
RL SUBUNIT. Interacts with CLK4.
CC 1- SUBUNIT. Interacts with CLK4.
CC 1- SUBCELLULAR LOCATION. Cytoplasmic.
CC 1- TISSUE SPECIFICITY. Ubiquitous. Highest level of expression in
CC heart, skeletal muscle, kidney, liver, iris and lymphoblasts.
CC 1- SIMILARITY. Contains 1 ubiquitin-like domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; AF313915; AAK14178.1; -; mRNA.
DR EMBL; EF007355; AAP36019.1; -; mRNA.
DR EMBL; BC007053; AAH07053.1; -; mRNA.
DR PDB; 1POR; NMR; A=1-73.
DR HGN; ENSG00000198258; Homo sapiens.
DR H-InvDB; HIX0014729; -.
DR MIM; 606849; -.
DR GO; GO:0005737; Cytoplasm; IDA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS0053; UBIQUITIN_2; FALSE NEG.
KW 3D-structure; Ub conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 100.0%; Score 394; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVKVCKNTDITGDLKKLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 60
Db |||||
QY 61 EIHGGMNLELYQ 73
Db |||||

RESULT 3
UBL5_MOUSE
ID UBL5_MOUSE STANDARD; PRT; 73 AA.
AC Q9EPV8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=Ubl5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RC STRAIN=C57BL/6J; TISSUE=Kidney, Pancreas, Spinal ganglion, and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee V., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AK002730; BAB22312.1; -; mRNA.
DR EMBL; AK003592; BAB23111.1; -; mRNA.
DR EMBL; AK007726; BAB25215.1; -; mRNA.
DR EMBL; AK009854; BAB26545.1; -; mRNA.
DR EMBL; AK012803; BAB28481.1; -; mRNA.
DR EMBL; AK051149; BAC34537.1; -; mRNA.
DR EMBL; BC028498; AAB28498.1; -; mRNA.
DR PDB; 1UH6; NMR; A=1-73.
DR MGI; MGI:1913427; Ub15.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS50053; UBIQUITIN_2; FALSE_NEG.
KW 3D-structure; Ub1 conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 100.0%; Score 394; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGTGRWNKIVLKKWYTIKDHVSLGDY 60
Db 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGTGRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYQ 73
Db 61 EIHGGMNLELYQ 73

RESULT 5
QSRC10_PONPY
ID QSRC10_PONPY PRELIMINARY; PRT; 73 AA.
AC QSRC10;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469G145.
GN Name=DKFZp469G145;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR58290; CAH90527.1; -; mRNA.
DR SNR; QSRC10; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.

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DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Psammomys obesus (Fat sand rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Gerbillinae; Psammomys.
OX NCBI_TaxID=48139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=20527879; PubMed=11078442;
RA Collier G.R., McMillan J.S., Windmill K., Walder K., Tenne-Brown J.,
RA de Silva A., Trevaskis J., Jones S., Morton G.J., Lee S., Augert G.,
RA Civitarese A., Zimet P.Z.;
RT "Beacon: a novel gene involved in the regulation of energy balance.";
RL Diabetes 49:1766-1771 (2000).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF318186; AAG34704.1; -; mRNA.
DR SNR; Q791B0; 1-73.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS50053; UBIQUITIN_2; FALSE_NEG.
KW Ub1 conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 100.0%; Score 394; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGTGRWNKIVLKKWYTIKDHVSLGDY 60
Db 1 MIEVNCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGTGRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYQ 73
Db 61 EIHGGMNLELYQ 73

RESULT 5
QSRC10_PONPY
ID QSRC10_PONPY PRELIMINARY; PRT; 73 AA.
AC QSRC10;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469G145.
GN Name=DKFZp469G145;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR58290; CAH90527.1; -; mRNA.
DR SNR; QSRC10; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.

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DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin, 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
DB 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
QY 61 EIHGGMNLELYQ 73
DB 61 EIHGGMNLELYQ 73

RESULT 6
Q4RSJ3 MACFA
ID Q4RSJ3_MACFA PRELIMINARY; PRT; 73 AA.
AC Q4RSJ3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Brain cDNA, clone: OFIA-12296, similar to human ubiquitin-like 5
DE (UBI5), (Testis cDNA, clone: QsA-15893, similar to human ubiquitin-
DE like 5 (UBI5)).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RA "DNA sequences of macaque genes expressed in brain or testis and its
RA evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RA "Substitution rate and structural divergence of 5'UTR evolution:
RA Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169550; BAB01632.1; -; mRNA.
DR EMBL; AB169533; BAB01034.1; -; mRNA.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Query Match 100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
DB 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
QY 61 EIHGGMNLELYQ 73
DB 61 EIHGGMNLELYQ 73

RESULT 7
UBLS BRARE
ID UBLS BRARE STANDARD; PRT; 73 AA.
AC Q7SXF2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Namesub15; ORFNames=zgc:66388;
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC 1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; BC055630; AAH55630.1; -; mRNA.
DR SMR; Q7SXF2; 1-72.
DR ZFIN; ZDB-GENE-040426-1629; zgc:66388.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin, 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS0053; UBIQUITIN_2; FALSE_NEG.
KW Ub1 conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8587 MW; 23716CB90FC7C545 CRC64;

Query Match 93.4%; Score 368; DB 1; Length 73;
Best Local Similarity 94.4%; Pred. No. 1.9e-34;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
DB 1 MIEVNCNDRLGKVRVKCNKNTDITIGDLKKLIAAQTGRNKKVILKKWYTFKDHVSLG DY 60
QY 61 EIHGGMNLELYQ 72
DB 61 EIHGGMNLELYQ 72

RESULT 8
Q5HZC1 XENLA
ID Q5HZC1_XENLA PRELIMINARY; PRT; 73 AA.
AC Q5HZC1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089084; AAH89084.1; -, mRNA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; Ubiquitin; 1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8635 MW; 2A51E123F36FF390 CRC64;
Query Match 93.1%; Score 367; DB 2; Length 73;
Best Local Similarity 91.8%; Pred. No. 2.4e-34;
Matches 67; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Db 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Qy 61 EIHGGMNLELYQ 73
Db 61 EIHGGMNLELYQ 73
RESULT 9
Q4SM16_TETNG
ID Q4SM16_TETNG PRELIMINARY; PRT; 73 AA.
AC Q4SM16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 18 SCAF14547, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00015743001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Doseat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype";
RL Nature 431:946-957 (2004).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB0101547; CAP98146.1; -, Genomic_DNA.
SQ SEQUENCE 73 AA; 8592 MW; 6A14CA0323F8E8EB CRC64;
Query Match 89.8%; Score 354; DB 2; Length 73;
Best Local Similarity 90.4%; Pred. No. 7.6e-33;
Matches 66; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Db 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Qy 61 EIHGGMNLELYQ 73
Db 61 EIHGGMNLELYQ 73
RESULT 10
Q7QHM2_ANOGA
ID Q7QHM2_ANOGA PRELIMINARY; PRT; 73 AA.
AC Q7QHM2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000015674.
GN ORFNames=ENSANG00000013185;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05206.2; -, Genomic_DNA.
DR SNR; Q7QHM2; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; Ubiquitin; 1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8599 MW; 43D212BE601B3C0D CRC64;
Query Match 87.3%; Score 344; DB 2; Length 73;
Best Local Similarity 83.6%; Pred. No. 1.1e-31;
Matches 61; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Db 1 MIEVVCNDRLGKGVKVCNTDDTTIGDLKLLIAAQTGRNKNVILKKWYTFKDHVSLG DY 60
Qy 61 EIHGGMNLELYQ 73
Db 61 EIHGGMNLELYQ 73

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RESULT 11
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ID UBLS_DROME STANDARD; PRT; 73 AA.
AC Q9V938; Q4QPS6;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name1(2)k03203; ORFNames=CG3450;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Rettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Berkley;
RA Stapleton M., Carlson J.W., Chavez C., Frise E., George R.A.,

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RA Pacle J.M., Park S., Wan K.H., Yu C., Celniker S.E.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB003790; AAF57398.1; -; Genomic_DNA.
CC EMBL; BT023690; AAY85090.1; -; mRNA.
CC SMR; Q9V938; 1-73.
CC Ensembl; CG3450; Drosophila melanogaster.
CC FlyBase; FBgn0022224; l(2)k03203.
CC GO; GO:0005737; Cytoplasm; ISS.
CC InterPro; IPR000626; Ubiquitin.
CC Pfam; PF00240; ubiquitin; 1.
CC PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
CC PROSITE; PS00553; UBIQUITIN_2; 1.
KW Ubiquitin-like.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8570 MW; 0870111AC5686A70 CRC64;
Query Match 86.0%; Score 339; DB 1; Length 73;
Best Local Similarity 86.3%; Pred. No. 4e-31; Indels 0; Gaps 0;
Matches 63; Conservative 3; Mismatches 7;
QY 1 MIEVNCNDRLGKVRKVCNDDTIGDLKKLIAAQTGRNKKVLFKQWYTFKDHVSLGDY 60
Db 1 MIEITCNDRLGKVRKVCNDDTIGDLKKLIAAQTGRNKKVLFKQWYTFKDHVSLGDY 60
QY 61 EIHGGMNLELYYQ 73
Db 61 EIHGGMNLELYYQ 73
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ID UBLS_CAEEL STANDARD; PRT; 73 AA.
AC P91302;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ubiquitin-like protein 5.
GN NameSubl-5; ORFNames=F46F11.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U88173; AAK21382.1; -; Genomic_DNA.
CC FAY; T25763; T25763.
CC SMR; P91302; 1-73.
CC Ensembl; F46F11.4; Caenorhabditis elegans.
CC WormBase; WBGene00006726; ubl-5.

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DR WormPep; F46F11.4; CE10602.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF0240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN 1; FALSE_NEG.
DR PROSITE; PS0053; UBIQUITIN 2; 1.
DR Complete proteome; Ub1 conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8738 MW; 61CA839BBA4006A4 CRC64;

Query Match 84.0%; Score 331; DB 1; Length 73;
Best Local Similarity 80.8%; Pred. No. 3.3e-30;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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Db 61 EIHEGFNFELYQ 73

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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein CBG14905.
GN Name=CBG14905;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.Briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC0100068; CAB68926.1; -; Genomic_DNA.
DR SNR; Q617M9; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF0240; ubiquitin; 1.
DR PROSITE; PS0053; UBIQUITIN_2; 1.
DR Hypothetical protein.
SQ SEQUENCE 73 AA; 8738 MW; 61CA839BBA4006A4 CRC64;

Query Match 84.0%; Score 331; DB 2; Length 73;
Best Local Similarity 80.8%; Pred. No. 3.3e-30;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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Qy 61 EIHGGMNLELYYQ 73
Db 61 EIHEGFNFELYQ 73

RESULT 14
Q5BS57 SCHJA PRELIMINARY; PRT; 73 AA.
AC Q5BS57;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;

RW NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY915407; AAX30628.1; -; mRNA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF0240; ubiquitin; 1.
DR PROSITE; PS0053; UBIQUITIN_2; 1.
DR Hypothetical protein.
SQ SEQUENCE 73 AA; 8679 MW; D3A862289A0B7CB5 CRC64;

Query Match 83.5%; Score 329; DB 2; Length 73;
Best Local Similarity 79.5%; Pred. No. 5.7e-30;
Matches 58; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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Db 61 EINDGMNLELYYQ 73

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madañ A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RG NTH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC096400; AAH96400.1; -; mRNA.
DR Hypothetical protein.
SQ SEQUENCE 73 AA; 8582 MW; 9B2C997752A6068 CRC64;

Query Match 82.5%; Score 325; DB 2; Length 73;
Best Local Similarity 83.6%; Pred. No. 1.6e-29;
Matches 61; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: April 8, 2006, 00:03:43 ; Search time 47 Seconds
(without alignments)
128.411 Million cell updates/sec

Title: US-10-067-832D-2
Perfect score: 394
Sequence: 1 MIEVVCNDRLGKVRKVCNT.....HVSIGDYEIHDGNWLELYQ 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	100.0	73	2	US-09-331-930A-2
2	394	100.0	73	2	US-09-331-930A-19
3	394	100.0	73	2	US-09-331-930A-20
4	394	100.0	73	2	US-09-331-930A-21
5	370	93.9	73	2	US-09-331-930A-24
6	354	89.8	73	2	US-09-331-930A-25
7	331	84.0	73	2	US-09-331-930A-22
8	286	72.6	66	2	US-09-331-930A-23
9	252	64.0	75	2	US-09-248-796A-16302
10	182	46.2	33	2	US-09-331-930A-16
11	182	46.2	33	2	US-09-331-930A-18
12	163	41.4	33	2	US-09-331-930A-14
13	80	20.3	60	2	US-09-331-930A-27
14	73.5	18.7	1078	2	US-09-583-110-4036
15	73.5	18.7	1080	2	US-09-107-433-4843
16	69	17.5	535	2	US-09-107-532A-6214
17	69	17.5	860	2	US-10-290-579A-252
18	66	16.8	921	2	US-09-902-540-15467
19	63.5	16.1	467	2	US-10-040-802-8
20	63.5	16.1	846	2	US-10-290-579A-249
21	63	16.0	374	2	US-09-248-796A-16046
22	63	16.0	533	2	US-09-248-796A-20066
23	61.5	15.6	842	2	US-10-290-579A-254
24	61	15.5	867	2	US-09-540-236-3193
25	60	15.2	475	2	US-09-248-796A-20067
26	60	15.2	482	2	US-09-270-767-43292
27	60	15.2	494	2	US-08-889-841B-19

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29	60	15.2	556	2	US-09-248-796A-18763	Sequence 18763, A
30	59.5	15.1	415	2	US-09-248-796A-14232	Sequence 14232, A
31	59.5	15.1	475	2	US-09-949-016-7954	Sequence 7954, Ap
32	59.5	15.1	493	2	US-09-411-628-10	Sequence 10, Appl
33	59.5	15.1	493	2	US-10-174-794-10	Sequence 10, Appl
34	59.5	15.1	629	2	US-09-107-532A-6656	Sequence 6656, Ap
35	59	15.0	157	2	US-09-248-796A-17780	Sequence 17780, A
36	59	15.0	440	2	US-09-540-236-2067	Sequence 2067, Ap
37	59	15.0	455	2	US-08-889-841B-46	Sequence 46, Appl
38	59	15.0	455	2	US-09-419-362-46	Sequence 46, Appl
39	59	15.0	850	1	US-08-448-603A-28	Sequence 28, Appl
40	59	15.0	850	2	US-09-134-075-28	Sequence 28, Appl
41	59	15.0	850	2	US-09-492-739-28	Sequence 28, Appl
42	59	15.0	850	2	US-09-966-931A-28	Sequence 28, Appl
43	58.5	14.8	353	2	US-09-248-796A-15778	Sequence 15778, A
44	58.5	14.8	498	2	US-08-889-841B-2	Sequence 2, Appl
45	58.5	14.8	498	2	US-08-889-841B-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-331-930A-2

; Sequence 2, Application US/09331930A

; Patent No. 6436670

; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.

; APPLICANT: COLLIER, GREGORY

; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR

; FILE REFERENCE: 22975-20007.00

; CURRENT APPLICATION NUMBER: US/09/331.930A

; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: PCT/AU98/00902

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: AU PP0117/97

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: AU PP0323/97

; PRIOR FILING DATE: 1997-11-11

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 73

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Amino acid

; OTHER INFORMATION: sequence for beacon from unknown organism

US-09-331-930A-2

Query Match .100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLG DY 60

Db 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLG DY 60

Qy 61 EIHGDNWLELYQ 73

Db 61 EIHGDNWLELYQ 73

RESULT 2

US-09-331-930A-19

; Sequence 19, Application US/09331930A

; Patent No. 6436670

; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.

; APPLICANT: COLLIER, GREGORY

; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR

; FILE REFERENCE: 22975-20007.00

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; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; TYPE: PRT
; LENGTH: 73
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-19

Query Match          100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYYQ 73
DB 61 EIHGGMNLELYYQ 73

RESULT 3
US-09-331-930A-20
; Sequence 20, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 73
; ORGANISM: Homo sapiens
US-09-331-930A-20

Query Match          100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYYQ 73
DB 61 EIHGGMNLELYYQ 73

RESULT 4
US-09-331-930A-21
; Sequence 21, Application US/09331930A
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; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-331-930A-21

Query Match          100.0%; Score 394; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYYQ 73
DB 61 EIHGGMNLELYYQ 73

RESULT 5
US-09-331-930A-24
; Sequence 24, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-331-930A-24

Query Match          93.9%; Score 370; DB 2; Length 73;
Best Local Similarity 93.1%; Pred. No. 8.8e-43;
Matches 67; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60
DB 1 MIEVVCNDRLGKVKVKNCTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIKDHVSLGDY 60

QY 61 EIHGGMNLELYY 72
DB 61 EIHGGMNLELYY 72
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Db 61 EIHGFMFELYQ 73

RESULT 8

US-09-331-930A-23

; Sequence 23, Application US/09331930A

; Patent No. 6436670

; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.

; APPLICANT: COLLIER, GREGORY

; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR

; FILE REFERENCE: 22975-20007.00

; CURRENT APPLICATION NUMBER: US/09/331.930A

; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: PCT/AU98/00902

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: AU PP0117/97

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: AU PP0323/97

; PRIOR FILING DATE: 1997-11-11

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Fasiola hepatica

US-09-331-930A-23

Query Match 72.6%; Score 286; DB 2; Length 66;

Best Local Similarity 81.8%; Pred. No. 2.le-31;

Matches 54; Conservative 5; Mismatches 7; Indels 0; Gaps 0

Qy 8 DRLGKVRVKCNTDDTIGDLKLLIAAQTGTRWNKIVLKQWYTFPKDHVSLGDIHOGMN 67

Db 1 DRLGKVRVKCNTPTDKVGDLLKLLIAAQTGAPRIVLKQWYTFPKDHVTLRDYEINDGMN 60

Qy 68 LELYQ 73

Db 61 LELYQ 66

RESULT 9

US-09-248-796A-16302

; Sequence 16302, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keth Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDID

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 16302

; LENGTH: 75

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-16302

Query Match 64.0%; Score 252; DB 2; Length 75;

Best Local Similarity 61.1%; Pred. No. 1e-26;

Matches 44; Conservative 12; Mismatches 16; Indels 0; Gaps 0

Qy 1 MIEVVCNDRLGKVRVKCNTDDTIGDLKLLIAAQTGTRWNKIVLKQWYTFPKDHVSLGDI 60

Db 3 MIEIQANDRLGKVIKLCLETDIGDVKKILGIQIGTFLEKILKGYQVYKHITLDDY 62

Qy 61 EIHGMMLELY 72

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Db 63 EIHDFNFELY 74

RESULT 10
US-09-331-930A-16
; Sequence 16, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-09-331-930A-16

Query Match 46.2%; Score 182; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 KIVLKKWYTFKDHVSLGDIYHIDGNLLEYQ 73
Db 1 KIVLKKWYTFKDHVSLGDIYHIDGNLLEYQ 33

RESULT 11
US-09-331-930A-18
; Sequence 18, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-09-331-930A-18

Query Match 46.2%; Score 182; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 KIVLKKWYTFKDHVSLGDIYHIDGNLLEYQ 73
Db 1 KIVLKKWYTFKDHVSLGDIYHIDGNLLEYQ 33

RESULT 12
US-09-331-930A-14
; Sequence 14, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-331-930A-14

Query Match 20.3%; Score 80; DB 2; Length 60;
Best Local Similarity 31.7%; Pred. No. 0.002;
Matches 19; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 11 GKKRVKCNDDTIGDLKKLIAAQGTGRWNKVLKKWYTFKDHVSLGDIYHIDGNLLEYQ 70
Db 1 GKTILEVSSDTIANVKEKIQVKEGKPDQMLIFPGQQLSDGVTLDGYDIHKKSTLYL 60

RESULT 13
US-09-331-930A-27
; Sequence 27, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-331-930A-27

Query Match 41.4%; Score 163; DB 2; Length 33;
Best Local Similarity 97.0%; Pred. No. 4.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIEVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33
Db 1 MIEVCNDRLGKVKVKNCTDDTIGDLKKLIAA 33

RESULT 14
US-09-583-110-4036
; Sequence 4036, Application US/09583110
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; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4036
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4036

Query Match      18.7%; Score 73.5; DB 2; Length 1078;
Best Local Similarity 32.8%; Pred. No. 0.61;
Matches 22; Conservative 9; Mismatches 27; Indels 9; Gaps 3;

Qy      13 KVRVKCNTDDTIGDLKLLIAAQTG---TRNKIV---LKKWYTIKDHVSLGDIYHIDGM 66
Db      140 KLRFKIKTDNKGVIKRVRIIEESGKRLWNSATTSKTKMQTIADYSPTLDV---DKI 198

Qy      67 NLELYYQ 73
Db      197 KLELFYE 203

RESULT 15
US-09-107-433-4843
; Sequence 4843, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4843:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1080 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1080
; SEQUENCE DESCRIPTION: SEQ ID NO: 4843:
US-09-107-433-4843
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Query Match      18.7%; Score 73.5; DB 2; Length 1080;
Best Local Similarity 32.8%; Pred. No. 0.61;
Matches 22; Conservative 9; Mismatches 27; Indels 9; Gaps 3;

Qy      13 KVRVKCNTDDTIGDLKLLIAAQTG---TRNKIV---LKKWYTIKDHVSLGDIYHIDGM 66
Db      142 KLRFKIKTDNKGVIKRVRIIEESGKRLWNSATTSKTKMQTIADYSPTLDV---DKI 198

Qy      67 NLELYYQ 73
Db      199 KLELFYE 205
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Search completed: April 8, 2006, 00:05:03
Job time : 48 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2006, 00:04:23 ; Search time 166 Seconds
(without alignments)
183.744 Million cell updates/sec

Title: US-10-067-832D-2
Perfect score: 394
Sequence: 1 MIEVVCNDRLGKVRKVCNT.....HVSIGDYEHGDMNLELYQ 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	100.0	73	5	US-10-067-832D-2
2	394	100.0	73	5	US-10-067-832D-15
3	394	100.0	73	5	US-10-067-832D-16
4	394	100.0	73	5	US-10-965-898-68
5	394	100.0	115	4	US-10-264-049-2463
6	370	93.9	73	5	US-10-067-832D-19
7	366	92.9	68	4	US-10-424-599-250542
8	354	89.8	73	5	US-10-067-832D-20
9	339	86.0	73	5	US-11-097-143-6522
10	331	84.0	73	5	US-10-067-832D-17
11	319	81.0	73	4	US-10-424-599-212296
12	312	79.2	73	4	US-10-437-963-147593
13	312	79.2	73	4	US-10-767-701-46049
14	312	79.2	73	4	US-10-425-115-233843
15	312	79.2	73	4	US-10-425-115-233846
16	312	79.2	73	4	US-10-425-115-233848
17	312	79.2	73	4	US-10-425-115-233849
18	312	79.2	73	4	US-10-425-115-233851
19	312	79.2	73	4	US-10-425-115-233853
20	311	78.9	73	4	US-10-425-115-288480
21	311	78.9	73	4	US-10-425-115-288482
22	311	78.9	73	4	US-10-425-115-288483
23	311	78.9	73	4	US-10-425-115-288486
24	304.5	77.3	74	4	US-10-424-599-207467
25	300	76.1	73	4	US-10-425-115-288481
26	285	72.6	66	5	US-10-067-832D-18
27	285	72.3	73	5	US-10-739-930-8461

28	281	71.3	73	4	US-10-425-115-288479
29	252	64.0	89	4	US-10-083-357-770
30	252	64.0	320	4	US-10-338-411-11
31	252	64.0	320	4	US-10-389-640-11
32	248	62.9	73	4	US-10-425-115-290033
33	246	62.4	89	4	US-10-425-115-355452
34	242	61.4	82	4	US-10-424-599-191611
35	234	59.4	71	4	US-10-424-599-147197
36	194	49.2	110	4	US-10-425-115-302543
37	184	46.7	70	4	US-10-425-115-302525
38	171	43.4	79	4	US-10-425-115-269824
39	170	43.1	63	4	US-10-424-599-229016
40	163	41.4	33	5	US-10-067-832D-14
41	160.5	40.7	93	4	US-10-424-599-266457
42	149	37.8	45	4	US-10-425-115-262612
43	138	35.0	27	3	US-09-864-761-41766
44	138	35.0	55	4	US-10-425-115-270723
45	131	33.2	59	4	US-10-425-115-356308

ALIGNMENTS

RESULT 1

US-10-067-832D-2
; Sequence 2, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEY
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067.832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Psammomys obesus
US-10-067-832D-2

Query Match 100.0%; Score 394; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MIEVVCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 60
Db	1	MIEVVCNDRLGKVRKVCNTDDTIGDLKLLIAAQTGRNKKIVLKKWYTFKDHVSLGDY 60

Qy	61	EIHGDMNLELYQ 73
Db	61	EIHGDMNLELYQ 73

RESULT 2

US-10-067-832D-15
; Sequence 15, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEY
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067.832D

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; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-832D-15

Query Match          100.0%; Score 394; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||
DB 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||

QY 61 EIHGGMNLELYQ 73
    |||||||
DB 61 EIHGGMNLELYQ 73
    |||||||

RESULT 3
US-10-067-832D-16
; Sequence 16, Application US/10067832D
; Publication No. US2005059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-067-832D-16

Query Match          100.0%; Score 394; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||
DB 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||

QY 61 EIHGGMNLELYQ 73
    |||||||
DB 61 EIHGGMNLELYQ 73
    |||||||

RESULT 4
US-10-965-898-68
; Sequence 68, Application US/10965898
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; Publication No. US20050084936A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Bandman, Olga
; Hillman, Jennifer L.
; Au-Young, Janice
; Tang, Y. Tom
; Yue, Henry
; Shah, Purvi
; Guegler, Karl J.
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/965,898
; FILING DATE: 18-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,403
; FILING DATE: 31-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0455 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT19
; CLONE: 3245954
; SEQUENCE DESCRIPTION: SEQ ID NO: 68 :
US-10-965-898-68

Query Match          100.0%; Score 394; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||
DB 1 MIEVVCNDRLGKRVKCNDDTIGDLKKLIAAQTGRNKNIVLKKWYTFKDHVSLGDY 60
    |||||||

QY 61 EIHGGMNLELYQ 73
    |||||||
DB 61 EIHGGMNLELYQ 73
    |||||||

RESULT 5
US-10-264-049-2463
; Sequence 2463, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
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; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2463
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2463

Query Match 100.0%; Score 394; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.6e-39;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHVSLG DY 60
Db 43 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHVSLG DY 102
Qy 61 EIHGGMNLELYY Q 73
Db 103 EIHGGMNLELYY Q 115

RESULT 6
US-10-067-832D-19
; Sequence 19, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1999-06-30
; PRIOR FILING DATE: 1998-10-30
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-067-832D-19

Query Match 93.9%; Score 370; DB 5; Length 73;
Best Local Similarity 93.1%; Pred. No. 1.2e-36;
Matches 67; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHVSLG DY 60
Db 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHITLAD Y 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMNLELYY 72

RESULT 7
US-10-424-599-250542
; Sequence 250542, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250542
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6826C.1.pcp
US-10-424-599-250542

Query Match 92.9%; Score 366; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.2e-36;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHVSLG DY 60
Qy 61 EIHGGMNLELYY 68
Db 61 EIHGGMNLELYY 68

RESULT 8
US-10-067-832D-20
; Sequence 20, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1999-06-30
; PRIOR FILING DATE: 1998-10-30
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-067-832D-20

Query Match 89.8%; Score 354; DB 5; Length 73;
Best Local Similarity 90.3%; Pred. No. 9.8e-35;
Matches 65; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHVSLG DY 60
Db 1 MIEVVCNDRLGKVRVKCNTDDTTIGDLKLLIAAQTGRWNKIVLKKWYTIKDHICLED Y 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMNLELYY 72

RESULT 9
US-11-097-143-6522
; Sequence 6522, Application US/11097143
; Publication No. US20050208558A1

GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,932
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6522
; LENGTH: 73
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6522

Query Match 86.0%; Score 339; DB 6; Length 73;
Best Local Similarity 86.3%; Pred. No. 6.2e-33;
Matches 63; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 MIEVNCNDRLGKVRVKCNCTDDTIGDLKKLIAAQTGTRNNKIVLKKWYTFKDHVSLG DY 60
DB 1 MIEITCNDRLGKVRVKCNPDPTIGDLKKLIAAQTGTRNNKIVLKKWYTFKDPRLSDY 60
QY 61 EIHGGMNLELYQ 73
DB 61 EIHGGMNLELYQ 73

RESULT 10
US-10-067-832D-17
; Sequence 17, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975200701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-832D-17

Query Match 84.0%; Score 331; DB 5; Length 73;
Best Local Similarity 80.8%; Pred. No. 5.7e-32;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 MIEVNCNDRLGKVRVKCNCTDDTIGDLKKLIAAQTGTRNNKIVLKKWYTFKDHVSLG DY 60
DB 1 MIEITVNDRLGKVRVKCNPSDTIGDLKKLIAAQTGTRNNKIVLKKWYTFKDHITLMDY 60
QY 61 EIHGGMNLELYQ 73
DB 61 EIHGGMNLELYQ 73
RESULT 11
US-10-424-599-212296
; Sequence 212296, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212296
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33729C.1.pap
US-10-424-599-212296
Query Match 81.0%; Score 319; DB 4; Length 73;
Best Local Similarity 81.9%; Pred. No. 1.6e-30;
Matches 59; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 MIEVNCNDRLGKVRVKCNCTDDTIGDLKKLIAAQTGTRNNKIVLKKWYTFKDHVSLG DY 60
DB 1 MIEVNLNDRLGKVRVKCNDDDTIGDLKKLIAAQTGTRADKIRIOKWYTYIKDHITLKDY 60
QY 61 EIHGGMNLELYQ 72
DB 61 EIHGGMNLELYQ 72
RESULT 12
US-10-437-963-147593
; Sequence 147593, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147593
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_48107C.1.pep
US-10-437-963-147593

Query Match 79.2%; Score 312; DB 4; Length 73;
Best Local Similarity 80.6%; Pred. No. 1.1e-29;
Matches 58; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKLLAAQTGTRWNKIVLKKWYTFKDHVSLGDY 60
Db 1 MIEVVLNDRLGKVRKVCNEDDTIGDLKLLVAAQTGTRPEKIRIQKWNYYKHITLKDY 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMLELYY 72

RESULT 13
US-10-767-701-46049
; Sequence 46049, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46049
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C594_1.pep
US-10-767-701-46049

Query Match 79.2%; Score 312; DB 4; Length 73;
Best Local Similarity 80.6%; Pred. No. 1.1e-29;
Matches 58; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKLLAAQTGTRWNKIVLKKWYTFKDHVSLGDY 60
Db 1 MIEVVLNDRLGKVRKVCNEDDTIGDLKLLVAAQTGTRPEKIRIQKWNYYKHITLKDY 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMLELYY 72

RESULT 14
US-10-425-115-233843
; Sequence 233843, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233843
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144858C.1.pep
US-10-425-115-233843

Query Match 79.2%; Score 312; DB 4; Length 73;
Best Local Similarity 80.6%; Pred. No. 1.1e-29;
Matches 58; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKLLAAQTGTRWNKIVLKKWYTFKDHVSLGDY 60
Db 1 MIEVVLNDRLGKVRKVCNEDDTIGDLKLLVAAQTGTRPEKIRIQKWNYYKHITLKDY 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMLELYY 72

RESULT 15
US-10-425-115-233846
; Sequence 233846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233846
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144860C.1.pep
US-10-425-115-233846

Query Match 79.2%; Score 312; DB 4; Length 73;
Best Local Similarity 80.6%; Pred. No. 1.1e-29;
Matches 58; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MIEVVCNDRLGKVRKVCNTDDTIGDLKLLAAQTGTRWNKIVLKKWYTFKDHVSLGDY 60
Db 1 MIEVVLNDRLGKVRKVCNEDDTIGDLKLLVAAQTGTRPEKIRIQKWNYYKHITLKDY 60
Qy 61 EIHGGMNLELYY 72
Db 61 EIHGGMLELYY 72

Search completed: April 8, 2006, 00:07:55
Job time : 167 secs

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OM protein - protein search, using sw model

Run on: April 8, 2006, 00:05:18 ; Search time 25 Seconds
(without alignments)
91.081 Million cell updates/sec

Title: US-10-067-832D-2
Perfect score: 394
Sequence: 1 MIEVVCNDRLGKVRVKCN.....HVSIGDYEHGHWLELYQ 73

Scoring table: BLOSUM62

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Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
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8: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65.5	16.6	860	7	US-11-100-356-6
2	65.5	16.6	867	7	US-11-100-356-3
3	65.5	16.6	869	7	US-11-100-356-4
4	60.5	15.4	1273	7	US-11-181-330-8
5	59	15.0	523	6	US-10-467-657-5392
6	58	14.7	654	6	US-10-510-947-6
7	57.5	14.6	662	7	US-11-072-512-3349
8	56.5	14.3	424	7	US-11-098-866-10445
9	56	14.2	377	7	US-11-096-568A-2441
10	56	14.2	379	7	US-11-096-568A-2440
11	56	14.2	731	7	US-11-024-959-421
12	55.5	14.1	258	7	US-11-058-924-6
13	55	14.0	306	7	US-11-052-554A-222
14	55	14.0	356	7	US-11-218-281-27
15	54.5	13.8	422	6	US-10-506-454-1192
16	54.5	13.8	454	7	US-11-087-099-6741
17	54.5	13.8	463	7	US-11-072-512-3058
18	54.5	13.8	842	7	US-11-100-356-2
19	54.5	13.8	1141	7	US-11-072-512-2522
20	54	13.7	50	6	US-10-467-657-8949
21	54	13.7	261	7	US-11-096-568A-5123
22	54	13.7	654	7	US-11-046-668-4
23	54	13.7	683	7	US-11-046-668-2
24	53.5	13.6	64	7	US-11-242-553-16
25	53.5	13.6	181	7	US-11-072-512-2800

26	53.5	13.6	262	7	US-11-096-568A-32083	Sequence 32083, A
27	53.5	13.6	272	7	US-11-096-568A-21992	Sequence 21992, A
28	53.5	13.6	274	7	US-11-096-568A-17414	Sequence 17414, A
29	53.5	13.6	313	7	US-11-087-719-15	Sequence 15, Appl
30	53.5	13.6	320	7	US-11-096-568A-21991	Sequence 21991, A
31	53.5	13.6	323	7	US-11-087-719-14	Sequence 14, Appl
32	53.5	13.6	324	7	US-11-096-568A-17413	Sequence 17413, A
33	53.5	13.6	338	7	US-11-087-719-13	Sequence 13, Appl
34	53.5	13.6	339	6	US-10-821-234-1507	Sequence 1507, Ap
35	53.5	13.6	339	7	US-11-072-175-143	Sequence 143, App
36	53.5	13.6	525	6	US-10-501-035-364	Sequence 364, App
37	53.5	13.6	701	7	US-11-096-568A-33795	Sequence 33795, A
38	53.5	13.6	920	7	US-11-087-099-11404	Sequence 11404, A
39	53	13.5	386	7	US-11-087-099-2197	Sequence 2197, App
40	53	13.5	655	7	US-11-072-175-199	Sequence 199, App
41	53	13.5	729	7	US-11-096-568A-27562	Sequence 27562, A
42	53	13.5	798	7	US-11-096-568A-27561	Sequence 27561, A
43	53	13.5	852	7	US-11-009-063-29	Sequence 29, Appl
44	53	13.5	892	7	US-11-096-568A-27560	Sequence 27560, A
45	52.5	13.3	269	6	US-10-821-234-1308	Sequence 1308, Ap

ALIGNMENTS

RESULT 1
US-11-100-356-6
; Sequence 6, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-11-100-356-6

Query Match	16.6%	Score 65.5;	DB 7;	Length 860;
Best Local Similarity	32.9%	Pred. No. 4.2;		
Matches	26;	Conservative	11;	Mismatches 23; Indels 19; Gaps 6;
Qy	2	IEVVC---NDRLGKVRVKCN-----TDDTIGDLKLLIAAQTGRWNKI---VLKKRY-- 48		
Db	294	VEINCRPNNTNRVIGPGQAFYATNDIIGNROAHNCNISTDRMKNKTLQVNMKQLQEH 353		
Qy	49	-----TI-FKHVSLGDYEI 62		
Db	354	FPNKTIRKFPHAG-GDLEI 371		

RESULT 2
US-11-100-356-3
; Sequence 3, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B


```

; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/385,704
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/427,752
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Murine leukemia virus
US-10-510-947-6

Query Match      14.7%; Score 58; DB 6; Length 654;
Best Local Similarity 34.3%; Pred.No.27;
Matches 12; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy      5 VCNDRLGKVRVKCNTDDTTIGDLKKLIAAOTGTRW 39
Db      373 LCMGAVKTHQALCNTTQSAGSGSYLLAAPTGTNW 407
          : : : : : : : : : : : : : : : : : :
          : : : : : : : : : : : : : : : : : :

RESULT 7
US-11-072-512-3349
; Sequence 3349, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3349
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3349

Query Match      14.6%; Score 57.5; DB 7; Length 662;
Best Local Similarity 30.3%; Pred.No.31;
Matches 23; Conservative 8; Mismatches 32; Indels 13; Gaps 3;

Qy      2 IEVVCNDRLGKVRVKCNTDDTTIGDLKKLIAAOTGTWNKIV-----LKKWTIIPK 52
Db      221 VDIATTEALSMQAEVDPEDGRTTIGILTKPOLVDKGTE-DKVVDPVRNLVFLHKKGYMIVK 279
          : : : : : : : : : : : : : : : : : :
          : : : : : : : : : : : : : : : : : :

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Qy  53 DHVSLGDYEHIDGMNL 68 .
Db  280 ---CRGQBIQDQLSL 292

RESULT 8
US-11-098-686-10445
; Sequence 10445, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10445
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10445

Query Match 14.3%; Score 56.5; DB 7; Length 424;
Best Local Similarity 25.3%; Pred. No. 25;
Matches 21; Conservative 9; Mismatches 24; Indels 29; Gaps

Qy  3 EVVCDNR--LGKVRVKCNMTDTIGDLKKLIAAQGTGRNKKVLKKWYTFKDHV-----
Db  335 EQAANDKTSLEKLIKKEKTNDCVGLKGSVMVSDG-----PFFPRDGVLDLCIN
Qy  56 -----SLGDYEHIDGMN 67
Db  384 QGVTAIQPGGSLNDYEVIKAVN 406

RESULT 9
US-11-096-568A-2441
; Sequence 2441, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2441
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 15221206
US-11-096-568A-2441

```

```

Query Match      14.2%; Score 56; DB 7; Length 377;
Best Local Similarity 30.8%; Pred. No. 25;
Matches 20; Conservative 9; Mismatches 18; Indels 18; Gaps 4;

Qy      19  NTDDTTGDLKLLTAAGTGRWN-----KIV-----LKKWYTIKDHVSLGDEYEH---DCM 66
          ||| :||| : : : : ||| : : : : : : : : : : : : : : : : : : :
Db      22  NTDGVGDIILKYLCKYQMGDRSLKVGKTPLEAAATVE-----DYELPKCKVDEF 75
          ||| :||| : : : : ||| : : : : : : : : : : : : : : : : : : :

Qy      67  NLELY 71
          ||| :||| : : : : ||| : : : : : : : : : : : : : : : : : : :

```

```
Db          76 NSEFY 80

RESULT 10
US-11-096-568A-2440
; Sequence 2440, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2440
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(379)
; OTHER INFORMATION: Ceres Seq. ID no. 15221205
US-11-096-568A-2440

Query Match          14.2%; Score 56; DB 7; Length 379;
Best Local Similarity 30.8%; Pred. No. 25;
Matches 20; Conservative 9; Mismatches 18; Indels 18; Gaps 4;

QY 19 NTDDTIGDLKKLIAAQTGRWN-----KIV-----LKKWYTFKDHVSLGDIETH---DGM 66
   ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 24 NTDGVVGDILRKYLCKYKQWDGRESLKIVGKTPLEAATIVE-----DYELPCRVDVF 77
   ||| :||: :||: :||: :||: :||: :||: :||: :||: :||:

QY 67 NLELY 71
   |||
Db 78 NSEFY 82

RESULT 11
US-11-024-959-421
; Sequence 421, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 421
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-421

Query Match          14.2%; Score 56; DB 7; Length 731;
Best Local Similarity 26.2%; Pred. No. 54;
Matches 11; Conservative 10; Mismatches 21; Indels 21; Gaps 0;

QY 7 NRRLGKKVRVKCNTDDTIGDLKKLIAAQTGRWNKIVLKKWY 48
   ||| :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 617 NDLLQENNLNCGTGHEPLVDLSSIDAIRNGNSILELIKDSWY 658
   ||| :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 12
US-11-058-924-6
; Sequence 6, Application US/11058924
; Publication No. US20060019308A1
; GENERAL INFORMATION:
; APPLICANT: Lund, Frances E.
; APPLICANT: Randall, Troy D.
; TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
; FILE REFERENCE: 13315/5
; CURRENT APPLICATION NUMBER: US/11/058,924
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 09/982,616
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/241,065
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 258
; TYPE: PRT
; ORGANISM: A. californica
US-11-058-924-6

Query Match          14.1%; Score 55.5; DB 7; Length 258;
Best Local Similarity 36.4%; Pred. No. 18;
Matches 12; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 IEVVCNDRLGKVRVKCNTDDTIGDLKKLIAAQ 34
   :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 190 VKVIVLHRLGKIEKCGAGSLL-DLEKLVKAK 221
   :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 13
US-11-052-554A-222
; Sequence 222, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus mutans UA159
US-11-052-554A-222

Query Match          14.0%; Score 55; DB 7; Length 306;
Best Local Similarity 26.1%; Pred. No. 26;
Matches 24; Conservative 12; Mismatches 26; Indels 30; Gaps 4;

QY 1 MIEVVCNDRLG-----KKVRVKCNTDDTIGDLKKLIAAQTGRWNKIVLKKWYT 49
   :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 6 LLLLVCLSLGLFACTSKKTADKLTVA-TNSIADITKNIAG-----NKKVLHSIVP 58
   :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 50 IFKD-----HVS LGDYEIHDGNLE 69
   :||: :||: :||: :||: :||: :||: :||: :||:
Db 59 VGRDPHEYPLEPDKVKTQADVIFYNGINLE 90
   :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 14
US-11-218-281-27
; Sequence 27, Application US/11218281
; Publication No. US20060024758A1
```

```
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; APPLICANT: Arita, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; TITLE OF INVENTION: RECEPTORS FOR ECOSAPENTAENOIC ACID ANALOGS
; FILE REFERENCE: MP-14448.05
; CURRENT APPLICATION NUMBER: US/11/218,281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 356
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-27

Query Match      14.0%; Score 55; DB 7; Length 356;
Best Local Similarity 20.4%; Pred.No. 31;
Matches 19; Conservative 17; Mismatches 29; Indels 28; Gaps 4;

QY      6 CNDK-----LGKKVRVKCNTDDTIGDLKKL-----IAAQTGTRWNKIVLKKWYT 49
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:
Db      11 CSDRQPGVLRDRSCSRKMSGCLSEVSLRPLTVVILSASIVVGVLGNGLVL---WMT 68
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:

QY      50 IFK-----DHVSLGDGYEIHGNNLELY 72
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:
Db      69 VFRMARTVSTVCFHFLALADFMLSLSLPIAMY 101
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:

RESULT 15
US-10-506-454-1192
; Sequence 1192, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1192
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1192

Query Match      13.8%; Score 54.5; DB 6; Length 422;
Best Local Similarity 38.3%; Pred.No. 44;
Matches 18; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

QY      9 RLGGKYR-VKCNDDTIGDLKKLIAAQTGTRWNKIVLKKWYTFKDH 54
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:
Db      178 RVGKPKVDKPTSDDP-----AAARTAEIVNEFV-RKAYEVLKDH 216
      |||      :|:      :|:      :|:      :|:      :|:      :|:      :|:

Search completed: April 8, 2006, 00:08:26
Job time : 26 secs
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:31:58 ; Search time 8.77373 Seconds
(without alignments)
1021.610 Million cell updates/sec

Title: US-10-067-832D-13

Perfect score: 188

Sequence: 1 atgatcgaggtgtgttgcga.....agaagctgattgcagcctaa 102

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool/US10067832/runat_07042006_175609_9682/app_query.fasta.1
-DB=A Geneseq -QFMT=fastan -SURFIX=n2p.rag -MINMATCH=0.1 -LOOPC1=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10067832 @CGN 1.1 476 @runat_07042006_175609_9682 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq 21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	86.7	33	2 AAY08414	Human bea
2	163	86.7	33	8 ADR43346	Human Bea
3	163	86.7	73	2 AAY08413	AAY08413 P. obesus
4	163	86.7	73	3 AAB36290	AAB36290 Israeli s
5	163	86.7	73	4 AAM39680	Human pol
6	163	86.7	89	4 AAM41466	Human pol
7	163	86.7	115	5 ABP41331	Human ova
8	152	80.9	73	4 AAB59910	Drosophila
9	147.5	78.5	32	3 AAB36291	Human bea

10	146	77.7	73	3 AAG40885	Zea mays
11	146	77.7	73	3 AAG41925	Arabidops
12	146	77.7	96	3 AAG41924	Arabidops
13	141	75.0	73	3 AAG27281	Zea mays
14	130.5	69.4	73	8 ADT58384	Plant pol
15	114	60.6	32	9 ADV95409	Yeast ubi
16	114	60.6	40	9 ADV95411	Yeast ubi
17	114	60.6	89	5 ADH32312	Novel yea
18	114	60.6	320	6 ABR83620	HUB1-GFP
19	86	45.7	104	5 ADH32742	Yeast smQ
20	83	44.1	110	8 ADY04784	Plant ful
21	83	44.1	112	8 ADY06931	Plant ful
22	83	44.1	112	8 ADX97089	Plant ful
23	83	44.1	112	8 ADX78384	Plant ful
24	83	44.1	113	8 ADY05953	Plant ful
25	83	44.1	124	8 ADY04557	Plant ful
26	83	44.1	128	8 ADX96955	Plant ful
27	73	38.8	123	8 ADY05551	Plant ful
28	73	38.8	125	8 ADY05562	Plant ful
29	68	36.2	27	4 AAM21187	Peptide #
30	68	36.2	27	4 ABB43508	Peptide #
31	68	36.2	27	4 AAM37402	Peptide #
32	68	36.2	27	4 ABB26468	Protein #
33	68	36.2	27	4 AAM77251	Human bon
34	68	36.2	27	4 AAM64443	Human bon
35	68	36.2	27	5 ABG46267	Human pep
36	59	31.4	92	7 ABO80827	Pseudomon
37	58	30.9	1447	3 AAB36514	Candida a
38	58	30.9	1447	5 ABP73835	Candida a
39	56.5	30.1	282	2 AAR34706	NAD cycla
40	56.5	30.1	282	2 AAR70095	NAD cycla
41	56.5	30.1	282	2 AAM80290	Aplysia c
42	55.5	29.5	261	9 ADU91841	Carbonic
43	55.5	29.5	2000	8 ADP24787	PRO poly
44	55.5	29.5	2000	9 ADY15157	PRO poly
45	55.5	29.5	2695	2 AAM07632	Human typ

ALIGNMENTS

RESULT 1

AAY08414

ID AAY08414 standard; protein; 33 AA.

XX AC AAY08414;

XX AC AAY08414;

DT 24-JUL-1999 (first entry)

XX Human beacon protein.

DE Human beacon protein.

XX Human beacon protein.

XX Human beacon protein.

KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;

KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;

KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;

KW medication; livestock; diagnosis; human.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 15

FT /label= unknown

FT /note= "encoded by CNC"

XX WO9923217-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-AU000902.

XX 31-OCT-1997; 97AU-00000117.

XX 11-NOV-1997; 97AU-00000323.

XX (TDDI-) INT DIABETES INST.

PA (UYDE-) UNIV DEAKIN.

XX Zimmet PZ, Collier G;
 XX WPI; 1999-337484/28.
 DR N-PSDB; AAX57370.
 XX New gene encoding a beacon protein associated with modulation of obesity,
 PT diabetes and metabolic energy levels.
 XX Claim 2; Page 54; 85pp; English.
 XX This invention describes a novel beacon protein and its encoding nucleic
 CC acid which is expressed in larger amounts in hypothalamus tissue of obese
 CC animals compared to lean animals. Agonists and antagonists of beacon can
 CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
 CC resistance. The beacon protein, itself is used to manufacture medicaments
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The
 CC treatment is contemplated for both human and animals, such as those
 CC important to the livestock industry. The antibody and polynucleotides are
 CC useful in diagnosis of conditions as above
 XX SQ Sequence 33 AA;

Alignment Scores:
 Pred. No.: 4.39e-15 Length: 33
 Score: 163.00 Matches: 33
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 86.7% Indels: 0
 DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x AAY08414 (1-33)

QY 1 ATGATCGAGGTGTTTTCGACGACCGTCTGGGAAAAGTCCNCGTTAAATCAACACG 60
 |||||
 Db 1 MetileGluValValCysAanAspArgLeuGlyLysLysVal**VallLysCysAsnThr 20
 QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
 |||||
 Db 21 AspAspThrileGlyAspLeuLysLysLeuileAala 33

RESULT 2
 ADR43346
 ID ADR43346 standard; peptide; 33 AA.

XX ADR43346;
 XX 04-NOV-2004 (first entry)
 XX Human Beacon protein.
 DE Beacon; Anorectic; Anabolic; Antidiabetic; Cytostatic; Cardiant;
 XX Antiinflammatory; Immunosuppressive; Antiinfertility; Neuroprotective;
 KW Nootropic; CLK; myopathy; obesity; anorexia; diabetes; cancer;
 KW heart disease; inflammation; Alzheimer's; Parkinson's; Pearson Syndrome;
 KW Pyruvate Carboxylase Deficiency; Pyruvate Dehydrogenase Deficiency;
 KW Cancer; Acoustic Neuroma; Acute Lymphocytic Leukemia; Carcinoma;
 KW Leukemia.
 XX Homo sapiens.
 XX W02004069866-A1.
 XX 19-AUG-2004.
 XX 10-FEB-2004; 2004WO-AU000147.
 XX 10-FEB-2003; 2003US-0446191P.
 XX (AUTO-) AUTOGEN RES PTY LTD.
 XX (UYDE-) UNIV DEAKIN.

PI Collier G, Walder K, Kerr-Bayles L;
 XX WPI; 2004-604412/58.
 XX New isolated ligands of mammalian or avian Beacon, useful for e.g.
 PT preventing or treating disorders associated with myopathy, obesity,
 PT diabetes, cancer, heart disease, inflammation, or disorders associated
 PT with the immune system.
 XX Claim 3; SEQ ID NO 4; 194pp; English.

XX The present invention relates to an isolated ligand of mammalian or avian
 CC Beacon or a homolog or derivative of the Beacon. The composition
 CC (including the agent capable of modulating the interaction between a
 CC Beacon and a CLK) or methods are useful for manufacturing a medicament
 CC for the treatment of a condition characterized by a healthy or unhealthy
 CC state, including the presence or absence of a disorder associated with
 CC myopathy, obesity, anorexia, weight maintenance, diabetes, disorders
 CC associated with mitochondrial dysfunction, genetic disorders, cancer,
 CC heart disease, inflammation, disorders associated with the immune system,
 CC infertility, disease associated with the brain and/or metabolic energy
 CC levels. The disease is selected from Alzheimer's, Parkinson's, diabetes,
 CC autism, and the aging process, LIC (Lethal Infantile Cardiomyopathy),
 CC sbgr;-oxidation Defects, COX Deficiency, Mitochondrial Cytopathy, Alper's
 CC Disease, Barth syndrome, Carnitine-Acyl-Carnitine Deficiency, Carnitine
 CC Deficiency, Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II
 CC Deficiency, Complex III Deficiency, Complex IV Deficiency, Complex V
 CC Deficiency, chronic progressive external ophthalmoplegia syndrome (CPEO),
 CC CPT I Deficiency, Glutaric Aciduria Type II, Kearns-Sayre syndrome (KSS),
 CC lactic acidosis, long-chain acyl-CoA dehydrogenase deficiency (LCAD),
 CC LCHAD, Leigh Disease, Leber Hereditary Optic Neuropathy (LHON), Luft
 CC Disease, mitochondrial DNA depletion, Mitochondrial Encephalopathy,
 CC Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase
 CC Deficiency, and the other diseases mentioned in the specification. The
 CC cancer is selected from ABL1 protooncogene, AIDS Related Cancers,
 CC Acoustic Neuroma, Acute Lymphocytic Leukemia, Acute Myeloid Leukemia,
 CC Adenocystic carcinoma, Adrenocortical Cancer, Agnogenic myeloid
 CC metaplasia, Alopecia, Alveolar soft-part sarcoma, Anal cancer,
 CC Angiosarcoma, Aplastic Anemia, Astrocytoma, Ataxia-telangiectasia, Basal
 CC Cell Carcinoma (Skin), Bladder Cancer, Bone Cancer, Bowel cancer, Brain
 CC Stem Glioma, Brain and CNS Tumours, Breast Cancer, CNS tumour, Carcinoid
 CC Tumours, Cervical Cancer, Childhood Brain Tumour, Childhood Cancer,
 CC Childhood Leukemia, and other cancers mentioned in the specification. The
 CC 11 sequences mentioned in the body of the specification do not correspond
 CC to the sequences represented in the SEQ ID listing.

XX SQ Sequence 33 AA;

Alignment Scores:
 Pred. No.: 4.39e-15 Length: 33
 Score: 163.00 Matches: 33
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 86.7% Indels: 0
 DB: 8 Gaps: 0

US-10-067-832D-13 (1-102) x ADR43346 (1-33)

QY 1 ATGATCGAGGTGTTTTCGACGACCGTCTGGGAAAAGTCCNCGTTAAATCAACACG 60
 |||||
 Db 1 MetileGluValValCysAanAspArgLeuGlyLysLysVal**VallLysCysAsnThr 20
 QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
 |||||
 Db 21 AspAspThrileGlyAspLeuLysLysLeuileAala 33

RESULT 3
 AAY08413
 ID AAY08413 standard; protein; 73 AA.
 XX AAY08413;
 XX 24-JUL-1999 (first entry)

XX DE P. obeseus beacon protein.
 XX KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;
 XX KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;
 KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;
 KW medicament; livestock; diagnosis.
 XX OS Psammomys obesus.
 XX KW WO9923217-A1.
 XX PN 14-MAY-1999.
 XX PD 30-OCT-1998; 98WO-AU000902.
 XX PF 31-OCT-1997; 97AU-00000117.
 XX PR 11-NOV-1997; 97AU-00000323.
 XX XX (ITDI-) INT DIABETES INST.
 XX FA (UYDE-) UNIV DEAKIN.
 XX PI Zimmet PZ, Collier G;
 XX DR WPI; 1999-337484/28.
 XX DR N-ESDB; AAX57359.
 XX XX New gene encoding a beacon protein associated with modulation of obesity,
 PT diabetes and metabolic energy levels.
 XX PS Claim 2; Page 50; 85pp; English.
 XX CC This invention describes a novel beacon protein and its encoding nucleic
 CC acid which is expressed in larger amounts in hypothalamus tissue of obese
 CC animals compared to lean animals. Agonists and antagonists of beacon can
 CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,
 CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin
 CC resistance. The beacon protein, itself is used to manufacture medicaments
 CC for treatment of obesity, anorexia, energy imbalance or diabetes. The
 CC treatment is contemplated for both human and animals, such as those
 CC important to the livestock industry. The antibody and polynucleotides are
 CC useful in diagnosis of conditions as above
 XX SQ Sequence 73 AA;
 Alignment Scores:
 Pred. No.: 4.74e-15 Length: 73
 Score: 163.00 Matches: 32
 Percent Similarity: 97.0% Conservative: 0
 Best Local Similarity: 97.0% Mismatches: 1
 Query Match: 86.7% Indels: 0
 DB: 2 Gaps: 0
 US-10-067-832D-13 (1-102) x AAY08413 (1-73)
 Qy 1 ATGATCGAGGTGTTTGCACACCGTCTGGGAAAAGTCCNCGTTAAATGCAACACG 60
 Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
 Qy 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
 Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaAla 33
 RESULT 4
 AAB36290
 ID AAB36290 standard; protein; 73 AA.
 AC AAB36290;
 XX 23-FEB-2001 (first entry)
 DT 23-FEB-2001 (first entry)
 DE Israeli sand rat beacon ligand.
 XX

KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes;
 KW ligand.
 XX OS Psammomys obesus.
 XX KW WO200064931-A1.
 XX PD 02-NOV-2000.
 XX PF 19-APR-2000; 2000WO-AU000342.
 XX PR 23-APR-1999; 99AU-00009919.
 XX PR 24-MAR-2000; 2000AU-00006454.
 XX PA (AUTO-) AUTOGEN PTY LTD.
 XX PI Collier G, Walder K, Zimmet P;
 XX DR WPI; 2000-687311/67.
 XX DR N-ESDB; AAC81767.
 XX PT Ligand of beacon protein useful for treating obesity, anorexia, energy
 PT imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and
 XX insulin resistance.
 XX PS Claim 3; Fig 1; 67pp; English.
 XX CC The present invention is related to the isolation of a ligand known as
 CC beacon from the Israeli sand rat. Beacon is associated with the
 CC regulation of energy balance, and the protein, its coding sequence and
 CC analogues can be used in the treatment of diabetes, obesity, anorexia,
 CC energy imbalance, metabolic syndrome, dyslipidemia, hypertension and
 CC insulin resistance. In addition, they can be used in agriculture to
 CC produce leaner animals
 XX SQ Sequence 73 AA;
 Alignment Scores:
 Pred. No.: 4.74e-15 Length: 73
 Score: 163.00 Matches: 32
 Percent Similarity: 97.0% Conservative: 0
 Best Local Similarity: 97.0% Mismatches: 1
 Query Match: 86.7% Indels: 0
 DB: 3 Gaps: 0
 US-10-067-832D-13 (1-102) x AAB36290 (1-73)
 Qy 1 ATGATCGAGGTGTTTGCACACCGTCTGGGAAAAGTCCNCGTTAAATGCAACACG 60
 Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
 Qy 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
 Db 21 AspAspThrIleGlyAspLeuLysLeuIleAlaAla 33
 RESULT 5
 AAB39680
 ID AAB39680 standard; protein; 73 AA.
 XX AC AAB39680;
 XX 22-OCT-2001 (first entry)
 DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 2825.
 XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX OS Homo sapiens.

XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX PI Zhou P, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58836.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX PT as central nervous system injuries.
XX PS Example 4; SEQ ID NO 2825; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX CC encoded polypeptides (AM38642-AM42213) with nootropic,
XX CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders. Note: The sequence data for this patent did not form
XX CC part of the printed specification
XX SQ Sequence 73 AA;
Alignment Scores:
Pred. No.: 4.74e-15 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 4 Gaps: 0
US-10-067-832D-13 (1-102) x AAM39680 (1-73)
QY 1 ATGATCGAGGTGTTTTCGACACGACCGCTCTGGGGAAGGTCGTTAAATGCAACACG 60
Db 1 MetIleGluValValCysAsnArgLeuGlyLysValArgValLysCysAsnThr 20
QY 61 GATGATACCATCGGGGACCTTAAGAGCTGATTCAGCC 99
Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaAla 33
RESULT 6
ID AAM41466
ID AAM41466 standard; protein; 89 AA.
XX AC AAM41466;
XX

DT 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 6397.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX PI Zhou P, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI60622.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX PT as central nervous system injuries.
XX PS Example 2; SEQ ID NO 6397; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX CC encoded polypeptides (AM38642-AM42213) with nootropic,
XX CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders. Note: The sequence data for this patent did not form
XX CC part of the printed specification
XX SQ Sequence 89 AA;
Alignment Scores:
Pred. No.: 4.83e-15 Length: 89
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 4 Gaps: 0
US-10-067-832D-13 (1-102) x AAM41466 (1-89)
QY 1 ATGATCGAGGTGTTTTCGACACGACCGCTCTGGGGAAGGTCGTTAAATGCAACACG 60
|||||

Db 17 MetIleGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 36
Qy 61 GATGATACCATCGGGAGCTTAAGAGCTGATTGCAGCC 99
Db 37 AspAepThrIleGlyAspLeuLysLysLeuIleAlaAla 49
RESULT 7
ABP41331
ID ABP41331 standard; protein; 115 AA.
XX
AC ABP41331;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HACNC39, SEQ ID NO:2463.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ54408.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 2463; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory system disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 115 AA;
Alignment Scores:
Pred. No.: 4.95e-15 Length: 115
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 5 Gaps: 0
US-10-067-832D-13 (1-102) x ABP41331 (1-115)
Qy 1 ATGATCGAGTGTGTTTGCACGACCGCTCTGGGAAAAAGTCCNGTTAAATGCACACG 60
Db 43 MetIleGluValValCysAsnAspArgLeuGlyLysLysValArgValLysCysAsnThr 62
Qy 61 GATGATACCATCGGGAGCTTAAGAGCTGATTGCAGCC 99
Db 63 AspAepThrIleGlyAspLeuLysLysLeuIleAlaAla 75
RESULT 8
ABBS59910
ID ABBS59910 standard; protein; 73 AA.
XX
AC ABBS59910;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 6522.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL04013.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 6522; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX ABBS72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 73 AA;

Alignment Scores:
Pred. No.: 2.01e-13 Length: 73
Score: 152.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 80.9% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-13 (1-102) x ABB59910 (1-73)

QY 1 ATGATCGAGGTTCTTTGCAACGACCGTCTGGGAAAAGGTCNCGTTAAATGCAACACG 60
Dd 1 MetIleGluIleThrCysAsnAepArgLeuGlyLysLysValArgVallysCysAsnPro 20
QY 61 GATGATACCATCGGGGACCTTAAAGAGCTGATTGCAGCC 99
Dd 21 AspAspThrIleGlyAspLeuLysLeuLeuAlaAla 33

RESULT 9
AAB36291
ID AAB36291 standard; protein; 32 AA.
XX
AC AAB36291;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human beacon (short form) protein sequence.
XX
KW Israeli sand rat; beacon; obesity; NIDDM; energy balance; diabetes;
KW ligand; human.
XX
OS Homo sapiens.
XX
PN WQ2000064931-A1.
XX
PD 02-NOV-2000.
XX
PF 19-APR-2000; 2000WO-AU000342.
XX
PR 23-APR-1999; 99AU-00009919.
PR 24-MAR-2000; 2000AU-00006454.
XX
PA (AUTO-) AUTOGEN PTY LTD.
XX
PI Collier G, Walder K, Zimmet P;
XX
DR WPI; 2000-687311/67.
DR N-PSDB; AAC81770.
XX
XX
PT Ligand of beacon protein useful for treating obesity, anorexia, energy
PT imbalance, diabetes, metabolic syndrome, dyslipidemia, hypertension and
PT insulin resistance.
XX
PS Disclosure; Fig 1B; 67pp; English.
XX
XX
CC The present invention is related to the isolation of a ligand known as
CC beacon from the Israeli sand rat. Beacon is associated with the
CC regulation of energy balance, and the protein, its coding sequence and
CC analogues can be used in the treatment of diabetes, obesity, anorexia,
CC energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and
CC insulin resistance. In addition, they can be used in agriculture to
CC produce leaner animals
XX
SQ Sequence 32 AA;

Alignment Scores:
Pred. No.: 8.61e-13 Length: 32
Score: 147.50 Matches: 32

Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 0
Query Match: 78.5% Indels: 1
DB: 3 Gaps: 1

US-10-067-832D-13 (1-102) x AAB36291 (1-32)

QY 1 ATGATCGAGGTTCTTTGCAACGACCGTCTGGGAAAAGGTCNCGTTAAATGCAACACG 60
Dd 1 MetIleGluValValCysAsnAepArgLeuGlyLysLysVal***VallysCysAsnThr 20
QY 61 GATGATACCATCGGGGACCTTAAAGAGCTGATTGCAGCC 99
Dd 21 AspAepThrIleGlyAspLeu---LysLeuIleAlaAla 32

RESULT 10
AAG40885
ID AAG40885 standard; protein; 73 AA.
XX
AC AAG40885;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 50790.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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PR 12-AUG-1999; 99US-0148341P.
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PR 07-SEP-1999; 99US-0152363P.
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PR 06-OCT-1999; 99US-0157865P.
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PR 12-OCT-1999; 99US-0158369P.
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PR 28-OCT-1999; 99US-0161992P.


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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1.6e-12 Length: 96
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservaive: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 3 Gaps: 0

US-10-067-832D-13 (1-102) x AAG41924 (1-96)

QY 1 ATGATCGAGTGTTCGACGACCGCTGGGGAAGGTCCNCGTTAATGCAACAGC 60
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QY 61 GATGATACCATCGGGGACCTTAAAGACTGATTCAGCC 99
Db 44 AspAspThrIleGlyAspLeuLysLysLeuValAlaAla 56

RESULT 13
AAG27281
ID AAG27281 standard; protein; 73 AA.
AC AAG27281;
XX
XX
XX 17-OCT-2000 (first entry)
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XX Zea mays protein fragment SEQ ID NO: 32055.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
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XX Zea mays subep. mays.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 25-OCT-1999; 99US-0161406P.
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PR 26-OCT-1999; 99US-0161361P.

PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 8,54e-12 Length: 73
Score: 141.00 Matches: 28
Percent Similarity: 87.9% Conservative: 1
Best Local Similarity: 84.8% Mismatches: 4
Query Match: 75.0% Indels: 0
DB: 3 Gaps: 0

US-10-067-832D-13 (1-102) x AAG27281 (1-73)

QY 1 ATGATCGAGGTGTTTGGCAACGACCTCTGGGGAAAAGTCNCCTTAATCAACACG 60
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QY 61 GATGATACCATCGGGGACCTTAAGAAAGCTGATTGCAGCC 99
Db 21 AspAepIhrIleGlyAspLeuAsnLysLeuValAlaAla 33

RESULT 14
ADTS8384
ID ADTS8384 standard; protein; 73 AA.
XX AC ADTS8384;
XX DT 13-JAN-2005 (first entry)
XX DE Plant polypeptide, SEQ ID 8461.
XX KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
disease resistance; galactomannan production; plant growth regulator;
heat tolerance; herbicide tolerance; lignin production;
extreme osmotic condition tolerance; pathogens resistance;
pest resistance; yield improvement; seed oil yield; seed protein yield.
XX OS Viridiplantae.
XX PN US2004216190-A1.
XX PD 28-OCT-2004.
XX PF 18-DEC-2003; 2003US-00739930.
XX PR 28-APR-2003; 2003US-00424599.
XX PR 28-APR-2003; 2003US-00425115.
XX PA (KOVA/) KOVALIC D K.
XX PI Kovalic DK;
XX DR WPI; 2004-757369/74.
XX PT New recombinant DNA constructs useful in the field of biochemistry and
genetics, and in particular for producing transgenic plants with improved
biological characteristics.
XX PS Claim 2; SEQ ID NO 8461; 14pp; English.
XX CC The invention relates a recombinant DNA construct comprising a
polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
(SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
Arabidopsis, wheat and rape but the specification does not indicate which
sequences is derived from which organism. Also included is a method of
producing a plant having an improved property, comprising transforming a
plant with a recombinant DNA construct comprising a promoter region
functional in a plant cell operably joined to a polynucleotide encoding a
polypeptide associated with the property, and growing the transformed
plant. The property is selected from improving plant cold tolerance, for
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CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.

XX Sequence 73 AA;

Alignment Scores:
Pred. No.: 3,06e-10 Length: 73
Score: 130.50 Matches: 28
Percent Similarity: 87.9% Conservative: 1
Best Local Similarity: 84.8% Mismatches: 3
Query Match: 69.4% Indels: 1
DB: 8 Gaps: 1

US-10-067-832D-13 (1-102) x ADF58384 (1-73)

QY 1 ATGATCAGGTGTTTTCACACGACCGTCTGGGAAAAGTCCNCGTTAATGCAACAG 60

Db 1 MetilegluValValLeuAsnAspArgLeuGlyLysLysValArgValLysCys----** 19

QY 61 GATGATACCATCGGGACCTTAGAACCTGATTCAGCC 99

Db 20 AspAspThrileGlyAspLeuLysLysLysValAlaAla 32

RESULT 15

ADV95409

ID ADV95409 standard; peptide; 32 AA.

XX AC ADV95409;

XX DT 07-APR-2005 (first entry)

XX DE Yeast ubiquitin like protein Hub1 amino terminal domain 1.

XX XW Fusion protein; protein folding; protein structure;

XX XW ubiquitin like protein.

XX OS Saccharomyces cerevisiae.

XX PN WO2005003313-A2.

XX PD 13-JAN-2005.

XX PF 28-JUN-2004; 2004WO-US020778.

XX PR 26-JUN-2003; 2003US-0482817P.

XX (LIFE-) LIFESENSORS INC.

XX PA Butt TR, Malakhov MP, Malakhova OA;

PI

XX

DR WPI; 2005-091798/10.

XX Enhancing expression of target protein in host cell, by expressing
XX nucleic acid construct containing sequences encoding carboxy-terminal
XX domain of ubiquitin-like molecule and target protein and encoding fusion
XX protein in host cell.

XX Example 7; SEQ ID NO 41; 107pp; English.

XX The invention relates to enhancing (M1) the expression of a protein of
XX interest in a host cell, involving expressing a nucleic acid construct
XX comprising a nucleic acid sequence encoding a carboxy-terminal domain of
XX a ubiquitin-like (Ubl) molecule and a protein of interest, where the
XX presence of the carboxy-terminal domain of the Ubl molecule in the fusion
XX protein increases expression level of protein of interest in the host
XX cell. Also included are producing (M2) a protein of interest (Involves
XX carrying out (M1), where the fusion protein, when expressed, comprises
XX the carboxy-terminal domain of Ubl molecule attached to the amino-
XX terminus of the protein of interest such that a cleavage site of the Ubl
XX molecule is immediately amino terminal to the protein of interest,
XX expressing the nucleic acid construct in the host cell, contacting the
XX expressed fusion protein with an amino-terminal domain of the same Ubl
XX molecule, thus generating a reconstituted Ubl, and contacting the
XX reconstituted Ubl with a protease specific to the Ubl molecule, thus
XX cleaving the fusion protein such that the protein of interest is now
XX produced), purifying (M3) the protein of interest (involving carrying out
XX specifically binding a purification tag (e.g. 6xHis tag or S-tag), and
XX contacting the purified reconstituted Ubl with a protease specific to the
XX Ubl molecule and cleaving the fusion protein such that the protein of
XX interest is now purified, or providing a nucleic acid construct which
XX encodes a fusion protein, containing a nucleic acid sequence encoding a
XX carboxy-terminal domain of Ubl molecule, the protein of interest, and a
XX first purification tag (attached to the amino-terminus of the carboxy-
XX terminal domain of a Ubl molecule) such that cleavage site of the Ubl
XX molecule is immediately amino terminal to the protein of interest,
XX expressing the nucleic acid construct encoding the fusion protein in the
XX host cell, purifying the fusion protein on a solid support capable of
XX specifically binding to the first purification tag, contacting the
XX purified fusion protein with an amino-terminal domain of the same Ubl
XX molecule comprising a second purification tag, thus generating a
XX reconstituted Ubl, purifying the reconstituted Ubl on a solid support
XX capable of specifically binding the second purification tag, and
XX contacting the purified reconstituted Ubl with a protease specific to the
XX Ubl molecule, thus cleaving the fusion protein such that the protein of
XX interest is now purified), increasing (M4) the affinity between a carboxy
XX -terminal domain of a Ubl molecule and a amino-terminal domain of a Ubl
XX molecule (involving operably linking a moiety to the carboxy-terminal and
XX to the amino-terminal domain, or inserting mutations into the carboxy-
XX terminal domain and the amino-terminal domain), a kit for purification of
XX a protein from a host cell, and generating an altered amino terminus in a
XX protein of interest in a host cell. The Ubl molecule is chosen from SUMO
XX (small ubiquitin related modifier), ubiquitin, RUB, HUB, APC8, APC12,
XX URM1, FAT10, Ubi-L and ISG15, preferably SUMO. The purification tag is
XX chosen from polyhistidine tag (6x His), polyarginine tag, glutathione-S-
XX transferase (GST), maltose binding protein (MBP), S-tag, influenza virus
XX HA tag, thioredoxin, staphylococcal protein A tag, the FLAG epitope,
XX AviTag epitope, and the c-myc epitope. The methods are useful for
XX enhancing the expression of a protein of interest in a host cell chosen
XX from yeast cell, Escherichia coli, bacterial cell, mammalian cell and
XX insect cell. The yeast SUMO N terminus is designated NTHS (N-terminal
XX half of SUMO) and the C-terminus CTHS. The present sequence represents a
XX ubiquitin like protein (or its N- or C-terminus) suitable for use in a
XX fusion protein of the invention.

XX Sequence 32 AA;

Alignment Scores:

Pred. No.: 7,81e-08 Length: 32
Score: 114.00 Matches: 21
Percent Similarity: 84.4% Conservative: 6
Best Local Similarity: 65.6% Mismatches: 5

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:39:29 ; Search time 1.62076 Seconds
(without alignments)
1211.048 Million cell updates/sec

Title: US-10-067-832D-13
Perfect score: 188
Sequence: 1 atgatcagaggtgttttgcac.....agaagctgattgcagcctaa 102

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	75.5	73	2 T47458	hypothetical prote
2	140	74.5	73	2 T40200	ubiquitin-like pro
3	135	71.8	73	2 T25763	hypothetical prote
4	114	60.6	73	2 S78735	protein YNR032c-a
5	56.5	30.1	282	2 S27769	NAD glycohydrolase
C 6	55.5	29.5	2695	2 S54974	type 1 inositol 1,
C 7	55.5	29.5	2713	2 A55713	inositol 1,4,5-tri
C 8	55.5	29.5	2734	2 B36579	inositol 1,4,5-tri
C 9	55.5	29.5	2749	1 A6MSIT	inositol 1,4,5-tri
C 10	55.5	29.5	2749	2 A36579	inositol 1,4,5-tri
C 11	54.5	29.0	2693	2 A40743	IP3 receptor, XIP3
C 12	52.5	27.9	831	2 A70363	mannose-1-phosphat
C 13	52.5	27.9	1170	2 S52525	probable membrane
C 14	52.5	27.9	2701	2 S17796	inositol-trisphosph

C 15	52	27.7	180	2 AC0197	conserved hypothet
C 16	52	27.7	371	2 A71359	conserved hypothet
C 17	52	27.7	1587	2 AB2012	hypothetical prote
C 18	52	27.7	1601	2 AB1730	hypothetical prote
C 19	52	27.7	4543	1 A53102	alpha-2-macroglobu
C 20	51.5	27.4	201	2 T31652	hypothetical prote
C 21	51	27.1	410	2 F96683	hypothetical prote
C 22	51	27.1	527	2 S42512	recombination-acti
C 23	51	27.1	662	2 T01857	hypothetical prote
C 24	51	27.1	3131	2 T39553	vacuolar protein 8
C 25	51	27.1	4544	1 S02392	alpha-2-macroglobu
C 26	51	27.1	4545	1 S25111	alpha-2-macroglobu
C 27	50.5	26.9	1290	2 A55094	chromosomal protei
C 28	50	26.6	69	2 A25161	tray protein - Sal
C 29	50	26.6	88	2 JC5203	outer membrane pro
C 30	50	26.6	90	2 B86560	9 kDa-Cysteine-ric
C 31	50	26.6	90	2 A72064	cysteine rich oxi
C 32	50	26.6	309	2 S66265	L-ascorbate peroxi
C 33	50	26.6	355	2 B97060	uncharacterized pr
C 34	50	26.6	459	2 T37677	hypothetical integ
C 35	50	26.6	525	2 B81859	phospholipase D-fa
C 36	50	26.6	968	2 C64691	type III restricti
C 37	50	26.6	972	2 C71826	hypothetical prote
C 38	49.5	26.3	498	2 AD0854	probable permease
C 39	49.5	26.3	829	2 S12858	vira protein - Agr
C 40	49.5	26.3	1209	2 T31657	reverse transcript
C 41	49.5	26.3	1965	2 S75200	fat protein - Syne
C 42	49	26.1	392	2 AE3382	nifs protein (impo
C 43	49	26.1	434	2 T49044	hypothetical prote
C 44	49	26.1	508	2 B81083	cardiolipin synthe
C 45	49	26.1	551	2 C84549	probable ubiquitin

ALIGNMENTS

RESULT 1

T47458 hypothetical protein T14D3.120 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T47458

R/Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.

Submitted to the Protein Sequence Database, February 2000

A/Reference number: Z24467

A/Accession: T47458

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-73 <JOR>

A/Cross-references: UNIPROT:Q9MU1; UNIPARC:UPI000000A81D7; EMBL:AL138649

C/Genetics:

A/Map position: 3

A/Note: T14D3.120

Alignment Scores: 1.48e-12 Length: 73
Pred. No.: 142.00 Matches: 28
Score: 90.9% Conservative: 2
Percent Similarity: 84.8% Mismatches: 3
Best Local Similarity: 75.5% Indels: 0
Query Match: 2 Gaps: 0
DB: 2

US-10-067-832D-13 (1-102) x T47458 (1-73)

QY 1 ATGATCGAGGTCTTTTGGCAACGACCTGTGGGAAAAAGGTCCTCGTTAAATGCAACACG 60

|||||

Db 1 MeillegluValValLeuLeuAspArgLeuGlyValValArgValValCysAsnGlu 20

QY 61 GATGATACCATCGGGACCTTAAAGAGCTGATTCGACCC 99

|||||

Db 21 GluAspThrIleGlyAspLeuLysLeuValAlaAala 33

RESULT 2

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:32:23 ; Search time 9.42203 Seconds
(without alignments)
1527.566 Million cell updates/sec

Title: US-10-067-832D-13
Perfect score: 188
Sequence: 1 atgatcgaggtgtttgtcaa.....agaagctgattgcagcctaa 102

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/abs/ABSSWEB.spool/US10067832/runat_07042006_175611_9700/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USR=US10067832 @CGN 1.1.580 @runat_07042006_175611_9700 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	86.7	47	2 Q5BJS1_RAT	Q5bjs1 rattus norv
2	163	86.7	73	1 UBL5_HUMAN	Q5bz11 homo sapien
3	163	86.7	73	1 UBL5_MESAU	Q5egx7 mesocricetu
4	163	86.7	73	1 UBL5_MOUSE	Q5epv8 mus musculu
5	163	86.7	73	1 UBL5_PSAOB	Q791b0 psammomya o
6	163	86.7	73	2 Q5RC10_PONEY	Q5rc10 pongo pygma
7	163	86.7	73	2 Q4R5J3_MACFA	Q4r5j3 macaca fasc
8	153	81.4	73	1 UBL5_BRARE	Q7sx12 brachydania
9	152	80.9	73	1 UBL5_DROME	Q5v998 drosophila
10	151	80.3	73	2 Q5H2C1_XENLA	Q5h2c1 xenopus lae
11	150	79.8	73	2 Q7QHM2_ANOGA	Q7qhm2 anopheles g
12	147	78.2	73	2 Q4SM16_TETNG	Q4sm16 tetraodon n
13	146	77.7	73	1 UBL5_ARATH	Q5fgz9 arabidopsis
14	146	77.7	73	2 Q6K220_ORYSA	Q6k220 oryza sativ
15	146	77.7	73	2 Q570V8_ARATH	Q570v8 arabidopsis
16	143	76.1	73	2 Q81545_PLAF7	Q81545 plasmodium

17	143	76.1	73	2	Q7RBW4_PLAYO	Q7rbw4 plasmodium
18	143	76.1	73	2	Q4YUJ7_FLABE	Q4yuj7 plasmodium
19	142	75.5	73	2	Q9MIU1_ARATH	Q9miu1 arabidopsis
20	140	74.5	73	1	HUB1_SCHPO	O94650 schizosacch
21	136	72.3	87	2	O540Q3_DICDI	O54q03 dictyosteli
22	135	71.8	73	1	UBL5_CAEEL	P91302 caenorhabdi
23	135	71.8	73	1	Q617M9_CAEBR	Q617m9 caenorhabdi
24	133	70.7	73	2	Q4P9W2_USTMA	Q4p9w2 ustilago ma
25	133	70.7	73	2	Q4MZ69_THEPA	Q4mz69 theileria p
26	133	70.7	76	2	Q4UBE9_THEAN	Q4ube9 theileria a
27	131	69.7	73	2	O5BS57_SCHJA	O5bs57 schistosoma
28	130	69.1	70	2	Q6CT04_YARLI	Q6ct04 yarrowia li
29	128	68.1	73	2	Q4VAF8_MOUSE	Q4vaf8 mus musculu
30	121	64.4	276	2	O5SM54_CRYNE	Q5sm54 cryptococcu
31	121	64.4	276	2	O5K8L5_CRYNE	Q5k8l5 cryptococcu
32	120	63.8	73	1	HUB1_DEBHA	Q5bup7 debaryomyce
33	117	62.2	73	1	HUB1_CANGA	O5fx17 candida gla
34	116	61.7	74	1	HUB1_KULULA	Q8cul2 kluyveromyc
35	116	61.7	79	2	Q6CU11_KULULA	Q6cul1 kluyveromyc
36	115	61.2	73	1	HUB1_ASHGO	Q756x3 ashbya goess
37	110	58.5	73	1	HUB1_YEAST	Q6g546 saccharomyc
38	96	51.1	79	2	O50P03_ENTHI	O50p03 entamoeba h
39	86	45.7	616	2	O5BCG2_EMENI	Q5bcg2 aspergillus
40	85	45.2	237	2	Q4I016_GIBZE	Q4i016 gibberella
41	69	36.7	239	2	Q52620_MAGGR	Q52620 magnaporthe
C 42	66	35.1	333	2	Q8A116_BACTN	Q8a116 bacteroides
C 43	64.5	34.3	1417	2	Q4S7P9_TETNG	Q4s7p9 tetraodon n
C 44	62	33.0	189	2	Q4WK6_ASPFU	O4wyk6 aspergillus
45	62	33.0	261	2	Q8X065_NEUCR	Q8x065 neurospora

ALIGNMENTS

RESULT 1						
Q5BJS1_RAT						
ID	Q5BJS1_RAT	PRELIMINARY;	PRT;	47	AA.	
AC	Q5BJS1;					
DT	10-MAY-2005 (TREMBlrel. 30, Created)					
DT	10-MAY-2005 (TREMBlrel. 30, Last sequence update)					
DE	LOC500954 protein.					
DE	LOC500954 protein.					
GN	Names:LOC500954;					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;					
OC	Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Brain;					
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahy J., Hulton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,					
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences";					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE.					

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RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091358; AAH91358.1; -, mRNA.
DR SMR; Q5BSU1; 1-47.
SQ SEQUENCE 47 AA; 5400 MW; B8FE50E31B325338 CRC64;

Alignment Scores:
Pred. No.: 4.18e-16 Length: 47
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x Q5BSU1_RAT (1-47)
QY 1 ATGATCGAGTGTGTTTGCACACGCTCTGGGAAAAGGTCNCGTTAAATGCACACG 60
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgVallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAAGAGCTGATTGCAGCC 99
Db 21 AspAspThrIleGlyAspLeuTysLysLeuIleAlaAla 33

RESULT 2
UBLS_HUMAN
ID _UBLS_HUMAN STANDARD; PRT; 73 AA.
AC Q9BZL1;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Names=UBL5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Iris;
RX MEDLINE=21100898; PubMed=11161819; DOI=10.1006/geno.2000.6439;
RA Friedman J.S., Koop B.F., Raymond V., Walter M.A.;
RT "Isolation of a ubiquitin-like (UBL5) gene from a screen identifying
highly expressed and conserved iris genes.";
RL Genomics 71:252-255(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Viallao D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP STRUCTURE BY NMR, AND INTERACTION WITH CLK4.
RX MEDLINE=22709234; PubMed=12824502; DOI=10.1110/ps.0382803;
RA McNally T., Huang Q., Janis R.S., Liu Z., Olejniczak E.T.,
RA Reilly R.M.;
RT "Structural analysis of UBL5, a novel ubiquitin-like modifier.";
RL Protein Sci. 12:1562-1566(2003).
CC -1- SUBUNIT: Interacts with CLK4.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest level of expression in
heart, skeletal muscle, kidney, liver, iris and lymphoblasts.
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; AF313915; AAK14178.1; -, mRNA.
DR EMBL; BT007355; AAP36019.1; -, mRNA.
DR EMBL; BC007053; AAH07053.1; -, mRNA.
DR FDB; lPOR; NMR; A=1-73.
DR Ensembl; ENSG00000198258; Homo sapiens.
DR HGNC; HGNC:13736; UBL5.
DR H-InvDB; HIX0014729; -.
DR MIM; 606849; -.
DR GO; GO:0005737; Cytoplasm; IDA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS0053; UBIQUITIN_2; FALSE NEG.
DR 3D-structure; Ubl conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
Pred. No.: 4.3e-16 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 1 Gaps: 0

US-10-067-832D-13 (1-102) x UBL5_HUMAN (1-73)
QY 1 ATGATCGAGTGTGTTTGCACACGCTCTGGGAAAAGGTCNCGTTAAATGCACACG 60
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysLysValArgVallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAAGAGCTGATTGCAGCC 99
Db 21 AspAspThrIleGlyAspLeuTysLysLeuIleAlaAla 33

RESULT 3
UBLS_MESAU
ID _UBLS_MESAU STANDARD; PRT; 73 AA.
AC Q6EGX7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Name=UBL5;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Cricetidae; Cricetinae; Mesocricetus.
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OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA "Beacon in the golden hamster."
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY329082; AAQ99044.1; -; mRNA.
DR SMR; Q6EGX7; 1-73.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS50053; UBIQUITIN_2; FALSE NEG.
KW UBL conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
Pred. No.: 4.3e-16 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 1 Gaps: 0

US-10-067-832D-13 (1-102) x UBL5_MESAU (1-73)
QY 1 ATGATCGAGGTGTTTCACAGCCGCTCGGGAAAGGTCNCGTAAATGCAACG 60
DB 1 MetleleluvalvaIcysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTCAGCC 99
DB 21 AspAspThrleIGlyAspLeuLysLeuIleAla 33

RESULT 4
UBL5 MOUSE STANDARD; PRT; 73 AA.
ID AC Q9EPV8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=Ubl5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney, Pancreas, Spinal ganglion, and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brubic V., Chothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

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RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takanaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wallesstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBUNIT: Interacts with CLK4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AK002730; BAB22312.1; -; mRNA.
DR EMBL; AK003992; BAB23111.1; -; mRNA.
DR EMBL; AK007726; BAB25215.1; -; mRNA.
DR EMBL; AK009854; BAB26545.1; -; mRNA.
DR EMBL; AK012803; BAB28481.1; -; mRNA.
DR EMBL; AK051149; BAC34537.1; -; mRNA.
DR EMBL; BC028498; AAB28498.1; -; mRNA.
DR PDB; 1UH6; NMR; A=1-73.
DR MGI; MGI:1913427; Ubl5.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE NEG.
DR PROSITE; PS50053; UBIQUITIN_2; FALSE NEG.
KW 3D-structure; Ubl conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:
Pred. No.: 4.3e-16 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 1 Gaps: 0

```

Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: Gaps: 0

US-10-067-832D-13 (1-102) x UBL5_MOUSE (1-73)

QY 1 ATGATCGAGTGTCTTTGCAACGACCGTCTGGGAAAAGGTCNCGTTAAATGCAACACG 60
|||||
DB 1 MetileGluValValCysAenAapAgLeuGlyLysLysValArgValLysCysAenThr 20
|||||
QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
|||||
DB 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaAla 33
|||||

RESULT 5

UBL5_PSAOB
ID UBL5_PSAOB STANDARD; PRT; 73 AA.
AC Q791B0;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5 (Beacon protein).
GN Names=UBL5;
OS Psammomys obesus (Fat sand rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Gerbillinae; Psammomys.
OX NCBI_TaxID=48139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=20527879; PubMed=11078442;
RA Collier G.R., McMillan J.S., Windmill K., Walder K., Tenne-Brown J.,
RA de Silva A., Trevaak J., Jones S., Morton G.J., Lee S., Augert G.,
RA Civitarese A., Zimmert P.Z.;
RT "Beacon: a novel gene involved in the regulation of energy balance.";
RL Diabetes 49:1766-1771(2000).
CC -|- SUBUNIT: Interacts with CLK4 (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Contains 1 ubiquitin-like domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; AF318186; AAG34704.1; -; mRNA.

DR SNR; Q791B0; 1-73.

DR InterPro; IPR000626; Ubiquitin.

DR Pfam; PF00240; ubiquitin.1.

DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.

DR PROSITE; PS00533; UBIQUITIN_2; FALSE_NEG.

KW Ub1 conjugation pathway.

FT DOMAIN 1 73 Ubiquitin-like.

SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:

Pred. No.: 4.3e-16 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 1
Best Local Similarity: 97.0% Mismatches: 0
Query Match: 86.7% Indels: 0
DB: Gaps: 1

US-10-067-832D-13 (1-102) x UBL5_PSAOB (1-73)

QY 1 ATGATCGAGTGTCTTTGCAACGACCGTCTGGGAAAAGGTCNCGTTAAATGCAACACG 60
|||||
DB 1 MetileGluValValCysAenAapAgLeuGlyLysLysValArgValLysCysAenThr 20
|||||

QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
|||||

Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaAla 33

RESULT 6

QSRC10_PONPY
ID QSRC10_PONPY PRELIMINARY; PRT; 73 AA.
AC QSRC10;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469G145.
GN Name=DKFZp469G145;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Ansorge W., Kleiger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858290; CAH90527.1; -; mRNA.
DR SNR; QSRC10; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin.1.
KW Hypothetical protein.

SQ SEQUENCE 73 AA; 8547 MW; D68BC941536AA39F CRC64;

Alignment Scores:

Pred. No.: 4.3e-16 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: Gaps: 2

US-10-067-832D-13 (1-102) x QSRC10_PONPY (1-73)

QY 1 ATGATCGAGTGTCTTTGCAACGACCGTCTGGGAAAAGGTCNCGTTAAATGCAACACG 60
|||||

Db 1 MetileGluValValCysAenAapAgLeuGlyLysLysValArgValLysCysAenThr 20
|||||

QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
|||||

Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAlaAla 33
|||||

RESULT 7

Q4R5J3_MACFA

ID Q4R5J3_MACFA PRELIMINARY; PRT; 73 AA.

AC Q4R5J3;

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Brain cDNA, clone: OFLA-12296, similar to human ubiquitin-like 5

DE (UBL5), (Testis cDNA, clone: QteA-15893, similar to human ubiquitin-

DE like 5 (UBL5)).

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecidae; Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA International consortium for macaque cDNA sequencing, analysis;

RT "DNA sequences of macaque genes expressed in brain or testis and its

RT evolutionary implications."

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Osada N., Hirata M., Tanuma R., Kueada J., Hida M., Suzuki Y.,

Qy	1	ATGATCGAGTGTGTTTGGCAACGACCGCTCTGGGGAAAAAGCTTCGCGTTAAATGCAACACG	80
Dd	1	MetileGluValValCysAenAepArgLeuGlyLyLeValArgVallyeCysAenGin	20
Qy	61	GATGATACCATCGGGGACCTTAAGAAGCTGATTGCAGCC	99
Dd	21	GluAepThrileGlyAspleuLyLyLeuileAlaAa	33
RESULT 9			
UBLS DROME			
ID	UBLS DROME	STANDARD;	PRT; 73 AA.
AC	Q9V938; Q4QPS6;		
DT	25-OCT-2004 (Rel. 45, Created)		
DT	25-OCT-2004 (Rel. 45, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Ubiquitin-like protein 5.		
GN	Name1(2)k03203; ORFNames=CG3450;		
OS	Drosophila melanogaster (fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Spheroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RR	[1]		
RP	NCBI_OTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RC	STRAIN=Berkely;		
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Adair J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,		
RA	Bailow R.M., Basu A., Bakendell J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,		
RA	Glocke A., Gong F., Gottlieb J.H., Gu Z., Guan P., Harris M.,		
RA	Harting N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hoskins D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milchins N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Stamps M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,		
RA	Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RT	"The genome sequence of Drosophila melanogaster."		
RL	Science 287:2185-2195 (2000).		
RL	[2]		
RP	GENOME REANNOTATION.		
RX	MEDLINE=22426069; PubMed=12537572;		
RA	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,		
RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,		
RA	Smith C.D., Tupay J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,		
RA	Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,		
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.		

RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation,";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05206.2; -; Genomic_DNA.
DR SMR; O7QHM2; 1-73.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS0053; UBIQUITIN 2; 1.
SQ SEQUENCE 73 AA; 8599 MW; 43D212BF601B3COD CRC64;

Alignment Scores:
Pred. No.: 4.69e-14 Length: 73
Score: 150.00 Matches: 28
Percent Similarity: 90.9% Conservative: 2
Best Local Similarity: 84.8% Mismatches: 3
Query Match: 79.8% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x Q7QHM2_ANOGA (1-73)
QY 1 ATGATCGAGGTTGTTTGCACACGCGTCTGGGGAAGAGTCNCGTTAAATGCAACACG 60
Db 1 MetileGluValThrCysAsnAspArgLeuGlyLysLysValA-gVallyeCysAanPro 20

QY 61 GATGATACCATCGGGGACCTTAAGAAGCTGATTGCAGCC 99
Db 21 AspAspThrIleGlyAspLeuLysLysLeuIleAla 33

RESULT 12
Q4SM16_TETNG
ID Q4SM16_TETNG PRELIMINARY; PRT; 73 AA.
AC Q4SM16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 18 SCAF14547, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00015743001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catalicio L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Nucleoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014547; CAF98146.1; -; Genomic_DNA.
FT NON TER 73
SQ SEQUENCE 73 AA; 8592 MW; 6A14CA0323F8E8EB CRC64;

Alignment Scores:
Pred. No.: 1.39e-13 Length: 73
Score: 147.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 78.2% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x Q4SM16_TETNG (1-73)
QY 1 ATGATCGAGGTTGTTTGCACACGCGTCTGGGGAAGAGTCNCGTTAAATGCAACACG 60
Db 1 MetileGluValThrCysAsnAspArgLeuGlyLysLysValA-gVallyeCysAanPro 20

QY 61 GATGATACCATCGGGGACCTTAAGAAGCTGATTGCAGCC 99
Db 21 GlnAspSerIleGlyAspLeuLysLysLeuIleAla 33

RESULT 13
UBL5_ARATH
ID UBL5_ARATH STANDARD; PRT; 73 AA.
AC Q9FGZ9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-like protein 5.
GN Name=UBL5; OrderedLocName=At5g42300; ORFNames=K5J14.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Kosemra E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers R., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tanase R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RL Science 302:842-846(2003).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AB023032; BAB10203.1; -; Genomic_DNA.
DR EMBL; AY072534; AAL66949.1; -; mRNA.
DR EMBL; AF370527; AAK48954.1; -; mRNA.
DR SNR; Q9FGZ9; 1-72.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
KW Ubl conjugation pathway.
FT DOMAIN 1 73 Ubiquitin-like.
SQ SEQUENCE 73 AA; 8571 MW; 4F20C6ED077133F6 CRC64;

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Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 1 Gaps: 0

US-10-067-832D-13 (1-102) x UBL5_ARATH (1-73)

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QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
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RESULT 14
Q6K220_ORYSA
ID Q6K220_ORYSA PRELIMINARY; PRT; 73 AA.
AC Q6K220;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Ubiquitin-like protein.
GN Name=B1469H02.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006168; BAD23730.1; -; Genomic_DNA.
DR SNR; Q6K220; 1-72.
DR Gramene; Q6K220; -.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
SQ SEQUENCE 73 AA; 8529 MW; FDA1C6ED0770F525 CRC64;

Alignment Scores:
Pred. No.: 1.99e-13 Length: 73
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x Q6K220_ORYSA (1-73)

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Db 21 AspAspThrIleGlyAspLeuLysLysLeuValAlaAa 33

RESULT 15

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ID Q570V8_ARATH PRELIMINARY; PRT; 73 AA.
AC Q570V8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Ubiquitin-like protein.
GN Name=At5g42300;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK220599; BAD94931.1; -; mRNA.
SQ SEQUENCE 73 AA; 8571 MW; 4F20C6ED077133F6 CRC64;

Alignment Scores:
Pred. No.: 1.99e-13 Length: 73
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x Q570V8_ARATH (1-73)

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QY 61 GATGATACCATCGGGACCTTAAGAGCTGATTGCAGCC 99
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Db 21 AspAspThrIleGlyAspLeuLysLysLeuValAlaAa 33

Search completed: April 7, 2006, 23:46:27
Job time : 52.1102 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:46:49 ; Search time 2.16102 Seconds
(without alignments)
780.458 Million cell updates/sec

Title: US-10-067-832D-13
Perfect score: 188
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	163	86.7	73	2	US-09-331-930A-2
3	163	86.7	73	2	US-09-331-930A-19
4	163	86.7	73	2	US-09-331-930A-20
5	163	86.7	73	2	US-09-331-930A-21
6	163	86.7	73	2	US-09-331-930A-24
7	163	86.7	73	2	US-09-331-930A-25
8	135	71.8	73	2	US-09-331-930A-22
9	106	56.4	66	2	US-09-331-930A-23
10	106	56.4	75	2	US-09-248-796A-16302
11	59	31.4	92	2	US-09-252-991A-29573
12	58	30.9	644	2	US-09-248-796A-17325

c 13	55.5	29.5	2713	4	PCT-US96-01735-1	Sequence 1, Appl
c 14	55.5	29.5	2749	2	US-09-385-222A-4	Sequence 4, Appl
c 15	54.5	29.0	456	2	US-09-328-352-6312	Sequence 6312, Ap
c 16	52.5	27.9	213	2	US-10-104-047-2722	Sequence 2722, Ap
c 17	52.5	27.9	1170	2	US-09-462-136-6	Sequence 6, Appl
c 18	52.5	27.9	2262	2	US-09-949-016-8849	Sequence 8849, Ap
c 19	52	27.7	222	2	US-09-252-991A-21885	Sequence 21885, A
c 20	52	27.7	231	2	US-09-107-532A-5301	Sequence 5301, Ap
c 21	52	27.7	1094	2	US-09-252-991A-32424	Sequence 32424, A
c 22	52	27.7	1094	2	US-09-268-347-32	Sequence 32, Appl
c 23	52	27.7	1761	2	US-09-489-039A-11234	Sequence 11234, A
c 24	51.5	27.4	487	2	US-10-012-231A-63	Sequence 63, Appl
c 25	51.5	27.4	487	2	US-10-015-389A-63	Sequence 63, Appl
c 26	51.5	27.4	487	2	US-10-006-768A-63	Sequence 63, Appl
c 27	51.5	27.4	487	2	US-10-015-71A-63	Sequence 63, Appl
c 28	51.5	27.4	487	2	US-10-015-393A-63	Sequence 63, Appl
c 29	51.5	27.4	487	2	US-10-011-833A-63	Sequence 63, Appl
c 30	51.5	27.4	487	2	US-10-006-041A-63	Sequence 63, Appl
c 31	51.5	27.4	487	2	US-10-012-064A-63	Sequence 63, Appl
c 32	51	27.1	4544	1	US-08-469-486-52	Sequence 52, Appl
c 33	51	27.1	4544	1	US-08-469-658-52	Sequence 52, Appl
c 34	50	26.6	90	2	US-09-198-452A-597	Sequence 597, App
c 35	50	26.6	92	2	US-09-438-185A-560	Sequence 560, App
c 36	50	26.6	221	2	US-09-270-767-48970	Sequence 48970, A
c 37	50	26.6	482	2	US-09-270-767-43252	Sequence 43252, A
c 38	50	26.6	512	2	US-09-270-767-42979	Sequence 42979, A
c 39	50	26.6	921	2	US-09-902-540-15467	Sequence 15467, A
c 40	49	26.1	113	2	US-09-173-300-54	Sequence 54, Appl
c 41	49	26.1	113	2	US-10-027-450-54	Sequence 54, Appl
c 42	49	26.1	302	2	US-09-270-767-44347	Sequence 44347, A
c 43	49	26.1	347	2	US-09-270-767-57323	Sequence 57323, A
c 44	49	26.1	348	2	US-09-248-796A-18141	Sequence 18141, A
c 45	49	26.1	349	2	US-09-270-767-42065	Sequence 42065, A

ALIGNMENTS

RESULT 1
US-09-331-930A-14
; Sequence 14, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMER, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCES: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: variable amino acid
US-09-331-930A-14

Alignment Scores:
Pred. No.: 4.25e-17 Length: 33
Score: 163.00 Matches: 33
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 86.7% Indels: 0
DB: 2 Gaps: 0

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Db 1 MetileGluValValCysAenAepArgLeuGlyLysVal***VallysCysAsnThr 20
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QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
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Db 21 AspAspThrileGlyAspleuLysLysLeuileAlaAla 33

RESULT 2
US-09-331-930A-2
; Sequence 2, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Unknown Organism
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-2
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Pred. No.: 4.8e-17 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
Gaps: 2
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Db 1 MetileGluValValCysAenAepArgLeuGlyLysVal***VallysCysAsnThr 20
  |||

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
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Db 21 AspAspThrileGlyAspleuLysLysLeuileAlaAla 33

RESULT 3
US-09-331-930A-19
; Sequence 19, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
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; ORGANISM: Unknown Organism
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-19
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Percent Similarity: 97.0% Conservative: 0
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Query Match: 86.7% Indels: 0
Gaps: 2
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QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
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Db 21 AspAspThrileGlyAspleuLysLysLeuileAlaAla 33

RESULT 4
US-09-331-930A-20
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; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Unknown Organism: Amino acid
; OTHER INFORMATION: sequence for beacon from unknown organism
US-09-331-930A-20
Alignment Scores:
Pred. No.: 4.8e-17 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
Gaps: 2
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QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
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RESULT 5
US-09-331-930A-21
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; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-331-930A-21
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Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x US-09-331-930A-21 (1-73)
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RESULT 6
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; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1997-11-11
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RESULT 7
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; Sequence 25, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
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; SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Saccharomyces cerevisiae
US-09-331-930A-25
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Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 2 Gaps: 0

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Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20

RESULT 8
US-09-331-930A-22
; Sequence 22, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
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; SEQ ID NO 22
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; TYPE: PRT
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US-09-331-930A-22
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Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 97.0% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x US-09-331-930A-22 (1-73)
Qy 1 ATGATCGAGGTGTTTTCACACGACCGTCTGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgValLysCysAsnThr 20
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-331-930A-22

Alignment Scores:
Pred. No.: 1,17e-12 Length: 73
Score: 135.00 Matches: 26
Percent Similarity: 84.8% Conservative: 2
Best Local Similarity: 78.8% Mismatches: 5
Query Match: 71.8% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x US-09-331-930A-22 (1-73)
QY 1 ATGATCGAGTGTGTTTGCACGACCGTCTGGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db 1 MetIleGluIleThrValAsnAspArgLeuGlyLysValArgIleLysCysAsnPro 20
QY 61 GATGATACCATCGGGGACCTTAAAGAGCTGATTGCAGCC 99
Db 21 SerAspThrIleGlyAspLeuLysLysLeuIleAlaAala 33

RESULT 9
US-09-331-930A-23
; Sequence 23, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Fasiola hepatica
US-09-331-930A-23

Alignment Scores:
Pred. No.: 4.01e-08 Length: 66
Score: 106.00 Matches: 21
Percent Similarity: 84.6% Conservative: 1
Best Local Similarity: 80.8% Mismatches: 4
Query Match: 56.4% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x US-09-331-930A-23 (1-66)
QY 22 GACCGTCTGGGAAAAAGTCCNCGTTAAATGCAACGATACCATCGGGACCTT 81
Db 1 AspArgLeuGlyLysLysValArgValLysCysAsnProThrAspLysValGlyAspLeu 20
QY 82 AAGAAGCTGATTGCAGCC 99
Db 21 LysLysLeuIleAlaAala 26

RESULT 10
US-09-248-796A-16302
; Sequence 16302, Application US/09248796A
; Patent No. 6747137
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; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16302
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16302

Alignment Scores:
Pred. No.: 4.09e-08 Length: 75
Score: 106.00 Matches: 19
Percent Similarity: 80.6% Conservative: 6
Best Local Similarity: 61.3% Mismatches: 6
Query Match: 56.4% Indels: 0
DB: 2 Gaps: 0

US-10-067-832D-13 (1-102) x US-09-248-796A-16302 (1-75)
QY 1 ATGATCGAGTGTGTTTGCACGACCGTCTGGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db 3 MetIleGluIleGlnAlaAenAspArgLeuGlyLysLysIleLysLeuLysCysLeuGlu 22
QY 61 GATGATACCATCGGGGACCTTAAAGAGCTGATT 93
Db 23 ThrAspThrIleGlyAspValLysLysIleLeu 33

RESULT 11
US-09-252-991A-29573
; Sequence 29573, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29573
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29573

Alignment Scores:
Pred. No.: 0.971 Length: 92
Score: 59.00 Matches: 10
Percent Similarity: 56.5% Conservative: 3
Best Local Similarity: 43.5% Mismatches: 8
Query Match: 31.4% Indels: 2
DB: 2 Gaps: 1

US-10-067-832D-13 (1-102) x US-09-252-991A-29573 (1-92)
QY 73 CGATGCTATCATCGGTGTTGCATTTAAACGNGGACCTTTTCCCCAGACGCGTCGTTGCAA 14
Db 58 ArgtrpSerArgProCysAlaValProAlaGlyProLeuAla-----AlaArgCysArg 75
QY 13 CAACTCGA 5
```

```
Db          76 AspProArg 78
|||||
RESULT 12
US-09-248-796A-17325
; Sequence 17325, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17325
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17325
Alignment Scores:
Pred. No.: 1.88 Length: 644
Score: 58.00 Matches: 12
Percent Similarity: 63.0% Conservative: 5
Best Local Similarity: 44.4% Mismatches: 10
Query Match: 30.9% Indels: 0
DB: 2 Gaps: 0
US-10-067-832D-13 (1-102) x US-09-248-796A-17325 (1-644)
QY 81 AAGTCCCGCATGATATCCGTTGTCATTTAACGNGGACCTTTTCCCGACGGTC 22
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Db 588 LysAlaProAspGlyLeuIlePheArgAlaPheAsnLysAsnTyrSerThrAspThrLeu 607
|||||
QY 21 GTTGCAAAACACCTCGATCAT 1
|||||
Db 608 ValMetThrSerLeuAspTyr 614
|||||
RESULT 13
PCT-US96-01735-1
; Sequence 1, Application PC/TUS9601735
; GENERAL INFORMATION:
; APPLICANT: Marks, Andrew R.
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01735
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/386,039
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kole, Lies B
; REGISTRATION NUMBER: 35,225
;
; REFERENCE/DOCKET NUMBER: A30042 - 165/30555
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2628
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2713 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
PCT-US96-01735-1
Alignment Scores:
Pred. No.: 5.77 Length: 2713
Score: 55.50 Matches: 14
Percent Similarity: 58.8% Conservative: 6
Best Local Similarity: 41.2% Mismatches: 11
Query Match: 29.5% Indels: 3
DB: 4 Gaps: 2
US-10-067-832D-13 (1-102) x PCT-US96-01735-1 (1-2713)
QY 96 TGCATCAGCTTCTTAAGTCCCGCATGATATCATCGTGTTCGATTTAACGNGGACCTT 37
Db 1398 CysAsnSerLeuLeuProLeu---AspAspIleValArgValValThrHisGluAspCys 1416
|||||
QY 36 TTTCGCCAGACGGTCGTTGCA-----AACAACTCGATCAT 1
|||||
Db 1417 IleProGluValIleAlaTyrIleAsnPheLeuAsnHis 1430
|||||
RESULT 14
US-09-385-222A-4
; Sequence 4, Application US/09385222A
; Patent No. 6465211
; GENERAL INFORMATION:
; APPLICANT: RIKEN;
; APPLICANT: Katsuhiko Mikoshiba
; TITLE OF INVENTION: High affinity IP3 binding polypeptide
; FILE REFERENCE: PH-657US
; CURRENT APPLICATION NUMBER: US/09/385,222A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: JP98/242207
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2749
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-385-222A-4
Alignment Scores:
Pred. No.: 5.78 Length: 2749
Score: 55.50 Matches: 14
Percent Similarity: 58.8% Conservative: 6
Best Local Similarity: 41.2% Mismatches: 11
Query Match: 29.5% Indels: 3
DB: 2 Gaps: 2
US-10-067-832D-13 (1-102) x US-09-385-222A-4 (1-2749)
QY 96 TGCATCAGCTTCTTAAGTCCCGCATGATATCATCGTGTTCGATTTAACGNGGACCTT 37
Db 1396 CysAsnSerLeuLeuProLeu---AspAspIleValArgValValThrHisGluAspCys 1414
|||||
QY 36 TTTCGCCAGACGGTCGTTGCA-----AACAACTCGATCAT 1
|||||
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Db      1415 IleProGluValLysIleAlaTyrIleAsnPheLeuAsnHis 1428
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RESULT 15
US-09-328-352-6312
; Sequence 6312, Application US/09328352
; Patent No: 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6312
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6312

Alignment Scores:
Pred. No.:      6.29      Length:      456
Score:          54.50      Matches:     11
Percent Similarity: 61.3%      Conservative: 8
Best Local Similarity: 35.5%      Mismatches: 9
Query Match:      29.0%      Indels:    3
DB:                2          Gaps:       1

US-10-067-832D-13 (1-102) x US-09-328-352-6312 (1-456)
Qy      84 CTTAGGTCCTCCGATCGT-----ATCATCGGTGTCATTAAACGGGACCTTTT 34
      ||:::|||||
Db      178 LeuArgLeuProAspGlyGluArgPheMetLeuArgPheAspArgAlaGluLeuAla 197
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Qy      33 CCCAGACGTCGTTCGAAACACCTCGATCAT 1
      ||::: |||
Db      198 ProArgAspIleValAlaArgThrIleAspHis 208
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Search completed: April 7, 2006, 23:49:31
Job time : 13.8051 secs

GenCore version 5.1.7

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 7, 2006, 23:48:08 ; Search time 7.41229 Seconds
 (without alignments)
 1149.944 Million cell updates/sec

Title: US-10-067-832D-13

Perfect score: 188

Sequence: 1 atgatcaggtgtgttgcaa.....agaagctgattgcagcctaa 102

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 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=15 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
 -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
 -USER=US10067832 @CGN 1 1 405 @runat_07042006_175617_9835 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMSOOT=120
 -WAE TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main:

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 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	163	86.7	33	5	US-10-067-832D-14
2	163	86.7	68	4	US-10-424-599-250542
3	163	86.7	73	5	US-10-067-832D-2
4	163	86.7	73	5	US-10-067-832D-15
5	163	86.7	73	5	US-10-067-832D-16
6	163	86.7	73	5	US-10-067-832D-19
7	163	86.7	73	5	US-10-067-832D-20
8	163	86.7	73	5	US-10-965-898-68
9	163	86.7	115	4	US-10-264-049-2463
10	152	80.9	73	6	US-11-097-143-6522
11	146	77.7	73	4	US-10-424-599-212296

12	146	77.7	73	4	US-10-437-963-147593
13	146	77.7	73	4	US-10-767-701-46049
14	146	77.7	73	4	US-10-425-115-233843
15	146	77.7	73	4	US-10-425-115-233846
16	146	77.7	73	4	US-10-425-115-233848
17	146	77.7	73	4	US-10-425-115-233849
18	146	77.7	73	4	US-10-425-115-233851
19	146	77.7	73	4	US-10-425-115-233853
20	146	77.7	73	4	US-10-425-115-288480
21	146	77.7	73	4	US-10-425-115-288482
22	146	77.7	73	4	US-10-425-115-288483
23	146	77.7	73	4	US-10-425-115-288486
24	140	74.5	73	4	US-10-425-115-288481
25	137	72.9	73	4	US-10-425-115-288479
26	135	71.8	73	5	US-10-067-832D-17
27	134	71.3	89	4	US-10-425-115-355452
28	131.5	69.9	74	4	US-10-424-599-207467
29	130.5	69.4	73	5	US-10-739-930-8461
30	120	63.8	45	4	US-10-425-115-262612
31	118	62.8	71	4	US-10-424-599-147197
32	114	60.6	89	4	US-10-083-357-770
33	114	60.6	320	4	US-10-338-411-11
34	111	60.6	320	4	US-10-389-640-11
35	110	58.5	73	4	US-10-424-599-191611
36	106	56.4	66	5	US-10-425-115-290033
37	97	51.6	55	4	US-10-425-115-270723
38	97	51.6	110	4	US-10-424-599-213543
39	93	49.5	83	4	US-10-437-963-135926
40	93	49.5	104	4	US-10-083-357-1200
41	86	45.7	59	4	US-10-425-115-356308
42	84	44.7	79	4	US-10-425-115-269824
43	84	44.7	178	4	US-10-437-963-149391
44	83	44.1	110	4	US-10-425-114-60599
45					

ALIGNMENTS

RESULT 1

US-10-067-832D-14
 ; Sequence 14, Application US/10067832D
 ; Publication No. US20050059108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZIMMET, PAUL ZEV
 ; APPLICANT: COLLIER, GREGORY
 ; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
 ; FILE REFERENCE: 229752000701
 ; CURRENT APPLICATION NUMBER: US/10/067,832D
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: PCT/AU98/00902
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: AU PP 0117
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: AU PP 0323
 ; PRIOR FILING DATE: 1997-11-11
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 14
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (15)
 ; OTHER INFORMATION: Leu, Pro, His, or Arg
 US-10-067-832D-14

Alignment Scores:
 Pred. No.: 4.98e-15 Length: 33
 Score: 163.00 Matches: 33
 Percent Similarity: 100.0% Conservative: 0

Sequence 147593,
 Sequence 46049, A
 Sequence 233843,
 Sequence 233846,
 Sequence 233848,
 Sequence 233849,
 Sequence 233851,
 Sequence 233853,
 Sequence 288480,
 Sequence 288482,
 Sequence 288483,
 Sequence 288486,
 Sequence 288481,
 Sequence 288479,
 Sequence 17, Appl
 Sequence 355452,
 Sequence 207467,
 Sequence 8461, Ap
 Sequence 262612,
 Sequence 147197,
 Sequence 770, App
 Sequence 11, Appl
 Sequence 191611,
 Sequence 290033,
 Sequence 270723,
 Sequence 213543,
 Sequence 135926,
 Sequence 1200, Ap
 Sequence 356308,
 Sequence 269824,
 Sequence 149391,
 Sequence 60599, A

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 86.7% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-067-832D-14 (1-33)

QY 1 ATGATCGAGGTGTTTTCACACGACCGTCTGGGAAAAAGGTCNCGTTAAATGCAACACG 60
|||||
DB 1 MetileGluValValCysAsnAspArgLeuGlyLysVal**VallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
|||||
DB 21 AspAspThrileGlyAspLeuLysLysLeuIleAlaAla 33

RESULT 2

US-10-424-599-250542
; Sequence 250542, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250542
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6826C.1.pep
US-10-424-599-250542

Alignment Scores:
Pred. No.: 5,32e-15 Length: 68
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-424-599-250542 (1-68)

QY 1 ATGATCGAGGTGTTTTCACACGACCGTCTGGGAAAAAGGTCNCGTTAAATGCAACACG 60
|||||
DB 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgVallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
|||||
DB 21 AspAspThrileGlyAspLeuLysLysLeuIleAlaAla 33

RESULT 3

US-10-067-832D-2
; Sequence 2, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323

; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Peamomomys obesius
US-10-067-832D-2

Alignment Scores:
Pred. No.: 5,36e-15 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-067-832D-2 (1-73)

QY 1 ATGATCGAGGTGTTTTCACACGACCGTCTGGGAAAAAGGTCNCGTTAAATGCAACACG 60
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DB 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgVallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
|||||
DB 21 AspAspThrileGlyAspLeuLysLysLeuIleAlaAla 33

RESULT 4

US-10-067-832D-15
; Sequence 15, Application US/10067832D
; Publication No. US20050059108A1
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL ZEV
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 229752000701
; CURRENT APPLICATION NUMBER: US/10/067,832D
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 09/331,930
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP 0117
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP 0323
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-832D-15

Alignment Scores:
Pred. No.: 5,36e-15 Length: 73
Score: 163.00 Matches: 32
Percent Similarity: 97.0% Conservative: 0
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 86.7% Indels: 0
DB: 5 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-067-832D-15 (1-73)

QY 1 ATGATCGAGGTGTTTTCACACGACCGTCTGGGAAAAAGGTCNCGTTAAATGCAACACG 60
|||||
DB 1 MetileGluValValCysAsnAspArgLeuGlyLysValArgVallysCysAsnThr 20

QY 61 GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC 99
|||||
DB 21 AspAspThrileGlyAspLeuLysLysLeuIleAlaAla 33

RESULT 5

Score:	163.00	Matches:	32
Percent Similarity:	97.0%	Conservative:	0
Best Local Similarity:	97.0%	Mismatches:	1
Query Match:	86.7%	Indels:	0
DB:	5	Gaps:	0

US-10-067-832D-13 (1-102) x US-10-067-832D-19 (1-73)

Qy	1	ATGATCGAGTTGTTTGGCAACGACCGTCTGGGGAAAAAGGTCCNCGTTAAATGCAACACG	60
Db	1	MetilegluValValCysAsnAspAglLeuGlyLysLysValArgValLysCysAsnThr	20
Qy	61	GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC	99
Db	21	AspAspThrileGlyAspLeuLysLysLeuIleAlaA1a	33

RESULT 7

US-10-067-832D-20

; Sequence 20, Application US/10067832D

; Publication No. US20050059108A1

; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL ZEV

; APPLICANT: COLLIER, GREGORY

; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR

; FILE REFERENCE: 229752000701

; CURRENT APPLICATION NUMBER: US/10/067,832D

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 09/331,930

; PRIOR FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: PCT/AU98/00902

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: AU PP 0117

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: AU PP 0323

; PRIOR FILING DATE: 1997-11-11

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 20

; LENGTH: 73

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-067-832D-20

Alignment Scores:			
Pred. No.:	5,36e-15	Length:	73
Score:	163.00	Matches:	32
Percent Similarity:	97.0%	Conservative:	0
Best Local Similarity:	97.0%	Mismatches:	1
Query Match:	86.7%	Indels:	0
DB:	5	Gaps:	0

US-10-067-832D-13 (1-102) x US-10-067-832D-20 (1-73)

Qy	1	ATGATCGAGTTGTTTGGCAACGACCGTCTGGGGAAAAAGGTCCNCGTTAAATGCAACACG	60
Db	1	MetilegluValValCysAsnAspAglLeuGlyLysLysValArgValLysCysAsnThr	20
Qy	61	GATGATACCATCGGGACCTTAAGAAGCTGATTGCAGCC	99
Db	21	AspAspThrileGlyAspLeuLysLysLeuIleAlaA1a	33

RESULT 8

US-10-965-898-68

; Sequence 68, Application US/10965898

; Publication No. US20050084936A1

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; Bandman, Olga

; Hillman, Jennifer L.

; Au-Young, Janice

; Tang, Y. Tom

; Yue, Henry

; Shah, Purvi

Qy 1 ATGATCAGGTTGTTTGCACACGCGTCTGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db |||||:|||||
1 MetileGluIleThrCysAsnAspArgLeuGlyLysValArgValLysCysAsnPro 20
Qy 61 GATGATACCATCGGGACCTTAAAGAAGCTGATTGCAGCC 99
Db |||||:|||||
21 AspaSpThrIleGlyAspLeuLysLysLeuIleAla 33

RESULT 11

US-10-424-599-212296
; Sequence 212296, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212296
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33729C.1.p
US-10-424-599-212296

Alignment Scores:
Pred. No.: 1.72e-12 Length: 73
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-424-599-212296 (1-73)

Qy 1 ATGATCAGGTTGTTTGCACACGCGTCTGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db |||||:|||||
1 MetileGluValValLeuAsnAspArgLeuGlyLysValArgValLysCysAsnAsp 20
Qy 61 GATGATACCATCGGGACCTTAAAGAAGCTGATTGCAGCC 99
Db |||||:|||||
21 AspaSpThrIleGlyAspLeuLysLysLeuValAla 33

RESULT 12

US-10-437-963-147593
; Sequence 147593, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147593
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48107C.1.p
US-10-437-963-147593

Alignment Scores:
Pred. No.: 1.72e-12 Length: 73
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-437-963-147593 (1-73)

Qy 1 ATGATCAGGTTGTTTGCACACGCGTCTGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db |||||:|||||
1 MetileGluValValLeuAsnAspArgLeuGlyLysValArgValLysCysAsnGlu 20
Qy 61 GATGATACCATCGGGACCTTAAAGAAGCTGATTGCAGCC 99
Db |||||:|||||
21 AspaSpThrIleGlyAspLeuLysLysLeuValAla 33

RESULT 13

US-10-767-701-46049
; Sequence 46049, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46049
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C594_1.p
US-10-767-701-46049

Alignment Scores:
Pred. No.: 1.72e-12 Length: 73
Score: 146.00 Matches: 29
Percent Similarity: 90.9% Conservative: 1
Best Local Similarity: 87.9% Mismatches: 3
Query Match: 77.7% Indels: 0
DB: 4 Gaps: 0

US-10-067-832D-13 (1-102) x US-10-767-701-46049 (1-73)

Qy 1 ATGATCAGGTTGTTTGCACACGCGTCTGGGAAAAAGTCCNCGTTAAATGCAACACG 60
Db |||||:|||||
1 MetileGluValValLeuAsnAspArgLeuGlyLysValArgValLysCysAsnGlu 20
Qy 61 GATGATACCATCGGGACCTTAAAGAAGCTGATTGCAGCC 99
Db |||||:|||||
21 AspaSpThrIleGlyAspLeuLysLysLeuValAla 33

RESULT 14

US-10-425-115-233843
; Sequence 233843, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147593
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa

Job time : 38.0614 secs

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; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233843
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144858C.1.pep
US-10-425-115-233843

Alignment Scores:
Pred. No.:      1.72e-12      Length:      73
Score:          146.00      Matches:      29
Percent Similarity: 90.9%      Conservative: 1
Best Local Similarity: 87.9%      Mismatches: 3
Query Match:      77.7%      Indels:      0
DB:              4          Gaps:      0

US-10-067-832D-13 (1-102) x US-10-425-115-233843 (1-73)

QY      1 ATGATCGAGTTGTTTGCACACGCGTCTCGGGAAAAAGGTCNCGTTAAATGCAACACG 60
Db      1 MetilegluValValleuAsnAspArgLeuGlyLysValArgValLysCysAsnGlu 20

QY      61 GATGATACCATCGGGACCTTAAGACGCTGATTGCAGCC 99
Db      21 AspAspThrileGlyAspLeuLysLeuValAlaAla 33

RESULT 15
US-10-425-115-233846
; Sequence 233846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233846
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144860C.1.pep
US-10-425-115-233846

Alignment Scores:
Pred. No.:      1.72e-12      Length:      73
Score:          146.00      Matches:      29
Percent Similarity: 90.9%      Conservative: 1
Best Local Similarity: 87.9%      Mismatches: 3
Query Match:      77.7%      Indels:      0
DB:              4          Gaps:      0

US-10-067-832D-13 (1-102) x US-10-425-115-233846 (1-73)

QY      1 ATGATCGAGTTGTTTGCACACGCGTCTCGGGAAAAAGGTCNCGTTAAATGCAACACG 60
Db      1 MetilegluValValleuAsnAspArgLeuGlyLysValArgValLysCysAsnGlu 20

QY      61 GATGATACCATCGGGACCTTAAGACGCTGATTGCAGCC 99
Db      21 AspAspThrileGlyAspLeuLysLeuValAlaAla 33
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(without alignments)
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Title: US-10-067-832D-13

Perfect score: 188

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Ygapop 10.0 , Ygapext 0.5
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Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 368322

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs02p
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELEX=6 -DELEXT=7

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2: /SID85/ptodata/1/pubpaa/US06 NEW PUB.pep.*
3: /SID85/ptodata/1/pubpaa/US07 NEW PUB.pep.*
4: /SID85/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
5: /SID85/ptodata/1/pubpaa/US09 NEW PUB.pep.*
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7: /SID85/ptodata/1/pubpaa/US11 NEW PUB.pep.*
8: /SID85/ptodata/1/pubpaa/US60_NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.5	30.1	258	7	US-11-058-924-6
2	52.5	27.9	213	7	US-11-072-512-2722
3	52	27.7	371	7	US-11-096-568A-5963
4	51.5	27.4	937	7	US-11-098-686-11296
5	51	27.1	37	6	US-10-957-351-107
6	51	27.1	4544	6	US-10-501-035-214
7	51	27.1	4544	7	US-11-076-427A-32
8	50	26.6	319	7	US-11-096-568A-17313
9	50	26.6	346	7	US-11-096-568A-17312

10	50	26.6	375	7	US-11-096-568A-17311
11	50	26.6	525	6	US-10-467-657-3462
12	49	26.1	3475	7	US-11-087-099-10885
13	49	26.1	3488	7	US-11-087-099-3005
14	48.5	25.8	1299	6	US-10-821-234-1145
15	48	25.5	47	7	US-11-004-399-3161
16	48	25.5	90	6	US-10-644-807-237
17	48	25.5	261	7	US-11-096-568A-5123
18	48	25.5	359	7	US-11-123-013-6
19	47	25.0	114	7	US-11-096-568A-31955
20	47	25.0	175	7	US-11-096-568A-31954
21	47	25.0	250	7	US-11-096-568A-30582
22	47	25.0	258	7	US-11-096-568A-30581
23	47	25.0	272	7	US-11-096-568A-30580
24	47	25.0	286	7	US-11-096-568A-31559
25	47	25.0	294	7	US-11-096-568A-31558
26	47	25.0	296	6	US-10-467-657-2024
27	47	25.0	308	7	US-11-096-568A-31557
28	47	25.0	355	7	US-11-087-099-3295
29	47	25.0	584	7	US-11-096-568A-31265
30	47	25.0	610	7	US-11-096-568A-31264
31	47	25.0	640	7	US-11-096-568A-31263
32	47	25.0	1126	7	US-11-075-185-3
33	46.5	24.7	274	7	US-11-087-099-6337
34	46.5	24.7	648	7	US-11-087-099-4135
35	46.5	24.7	964	7	US-11-103-957-13
36	46.5	24.7	964	7	US-11-018-868-19
37	46.5	24.7	1574	6	US-10-055-877-211
38	46	24.5	70	7	US-11-096-568A-1855
39	46	24.5	247	7	US-11-096-568A-29306
40	46	24.5	256	7	US-11-096-568A-29305
41	46	24.5	293	7	US-11-096-568A-16425
42	46	24.5	311	7	US-11-096-568A-29304
43	46	24.5	314	7	US-11-096-568A-19764
44	46	24.5	337	7	US-11-096-568A-19763
45	46	24.5	342	7	US-11-096-568A-19762

ALIGNMENTS

RESULT 1
US-11-058-924-6
; Sequence 6, Application US/11058924
; Publication No. US20060019308A1
; GENERAL INFORMATION:
; APPLICANT: Lund, Frances E.
; APPLICANT: Randall, Troy D.
; TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
; FILE REFERENCE: 13315/5
; CURRENT APPLICATION NUMBER: US/11/058,924
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 09/982,616
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/241,065
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 258
; TYPE: PRT
; ORGANISM: A. californica
US-11-058-924-6

Alignment Scores:
Pred No.: 0.867 Length: 258
Score: 56.50 Matches: 12
Percent Similarity: 62.5% Conservative: 8
Best Local Similarity: 37.5% Mismatches: 11
Query Match: 30.1% Indels: 1
DB: 7 Gaps: 1

US-10-067-832D-13 (1-102) x US-11-058-924-6 (1-258)

GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: C-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-107

Alignment Scores:
Pred. No.: 5.32 Length: 37
Score: 51.00 Matches: 10
Percent Similarity: 58.3% Conservative: 4
Best Local Similarity: 41.7% Mismatches: 10
Query Match: 27.1% Indels: 0
Gaps: 0
DB:

US-10-067-832D-13 (1-102) x US-10-957-351-107 (1-37)

Qy 7 GAGTTGTTTCAACGACCGTCTGGGAAAAGTCNCGTAAATGCAACCGATGAT 66

Db 5 GluPheGlnCysAsnAsnThrLeuCysLysProLeuAlaTrpLysCysAspGlyGluAep 24

Qy 67 ACCATCGGGAC 78

Db 25 AspCysGlyAep 28

RESULT 6

US-10-501-035-214
; Sequence 214, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-214

Alignment Scores:
Pred. No.: 8.59 Length: 4544
Score: 51.00 Matches: 10
Percent Similarity: 58.3% Conservative: 4
Best Local Similarity: 41.7% Mismatches: 10
Query Match: 27.1% Indels: 0
Gaps: 0
DB:

US-10-067-832D-13 (1-102) x US-10-501-035-214 (1-4544)

Qy 7 GAGTTGTTTCAACGACCGTCTGGGAAAAGTCNCGTAAATGCAACCGATGAT 66

Db 5 GluPheGlnCysAsnAsnThrLeuCysLysProLeuAlaTrpLysCysAspGlyGluAep 24

Db 3658 GluPheGlnCysAsnAsnThrLeuCysLysProLeuAlaTrpLysCysAspGlyGluAep 3677
Qy 67 ACCATCGGGAC 78
Db 3678 AspCysGlyAep 3681

RESULT 7

US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alicato, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOUS
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-32

Alignment Scores:
Pred. No.: 8.59 Length: 4544
Score: 51.00 Matches: 10
Percent Similarity: 58.3% Conservative: 4
Best Local Similarity: 41.7% Mismatches: 10
Query Match: 27.1% Indels: 0
Gaps: 0
DB:

US-10-067-832D-13 (1-102) x US-11-076-427A-32 (1-4544)

Qy 7 GAGTTGTTTCAACGACCGTCTGGGAAAAGTCNCGTAAATGCAACCGATGAT 66

Db 3658 GluPheGlnCysAsnAsnThrLeuCysLysProLeuAlaTrpLysCysAspGlyGluAep 3677

Qy 67 ACCATCGGGAC 78

Db 3678 AspCysGlyAep 3681

RESULT 8

US-11-096-568A-17313
; Sequence 17313, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17313
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(319)
; OTHER INFORMATION: Ceres Seq. ID no. 12357282
US-11-096-568A-17313

Alignment Scores:
Pred. No.: 9.5 Length: 319
Score: 50.00 Matches: 12
Percent Similarity: 63.3% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 7
Query Match: 26.6% Indels: 4
DB:

```
DB: 7 Gaps: 1
US-10-067-832D-13 (1-102) x US-11-096-568A-17313 (1-319)
QY 4 ATCGAGTGTGTTTGCACACGACCTCTGGGGAAGTCCNCGTTAAATGCAACACGGAT 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 IleAspLeuTyrTyrGlnHisArgIleAspLysValProIleGluVal----- 114
QY 64 GATACCATCGGGACCTTAAGACCTGATT 93
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---ThrIleGlyLeuLeuLysLysLeuVal 123
RESULT 9
US-11-096-568A-17312
; Sequence 17312, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17312
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(346)
; OTHER INFORMATION: Ceres Seq. ID no. 12357281
US-11-096-568A-17312
Alignment Scores:
Pred. No.: 9.57 Length: 346
Score: 50.00 Matches: 12
Percent Similarity: 63.3% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 7
Query Match: 26.6% Indels: 4
DB: 7 Gaps: 1
US-10-067-832D-13 (1-102) x US-11-096-568A-17312 (1-346)
QY 4 ATCGAGTGTGTTTGCACACGACCTCTGGGGAAGTCCNCGTTAAATGCAACACGGAT 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 IleAspLeuTyrTyrGlnHisArgIleAspLysValProIleGluVal----- 141
QY 64 GATACCATCGGGACCTTAAGACCTGATT 93
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 ---ThrIleGlyLeuLeuLysLysLeuVal 150
RESULT 10
US-11-096-568A-17311
; Sequence 17311, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17311
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(375)
; OTHER INFORMATION: Ceres Seq. ID no. 12357280
US-11-096-568A-17311
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Alignment Scores:
Pred. No.: 9.65 Length: 375
Score: 50.00 Matches: 12
Percent Similarity: 63.3% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 7
Query Match: 26.6% Indels: 4
DB: 7 Gaps: 1
US-10-067-832D-13 (1-102) x US-11-096-568A-17311 (1-375)
QY 4 ATCGAGTGTGTTTGCACACGACCTCTGGGGAAGTCCNCGTTAAATGCAACACGGAT 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 154 IleAspLeuTyrTyrGlnHisArgIleAspLysValProIleGluVal----- 170
QY 64 GATACCATCGGGACCTTAAGACCTGATT 93
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 ---ThrIleGlyLeuLeuLysLysLeuVal 179
RESULT 11
US-10-467-657-5462
; Sequence 5462, Application US/10467657
; Publication No. US20050260591A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5462
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5462
Alignment Scores:
Pred. No.: 9.98 Length: 525
Score: 50.00 Matches: 11
Percent Similarity: 56.5% Conservative: 2
Best Local Similarity: 47.8% Mismatches: 10
Query Match: 26.6% Indels: 0
DB: 6 Gaps: 0
US-10-067-832D-13 (1-102) x US-10-467-657-5462 (1-525)
QY 29 TGGGGAAGTCCNCGTTAAATGCAACACGATGATCCATCGGGGACCTTAAGAGC 88
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 TrpAlaSerHisSerAlaHisAlaThrArgIleArgSerGlyAsnIleGlyLys 258
QY 89 TGATTTCAG 97
|||:|||||:
Db 259 GlyLeuGln 261
RESULT 12
US-11-087-099-10885
; Sequence 10885, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10885
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; LENGTH: 3475
; TYPE: PRT
; ORGANISM: Nodularia spumigena
US-11-087-099-10885

Alignment Scores:
Pred. No.:      17.4      Length:      3475
Score:          49.00     Matches:      11
Percent Similarity: 62.1% Conservative: 7
Best Local Similarity: 37.9% Mismatches: 10
Query Match:      26.1% Indels:      1
DB:               7       Gaps:        0

US-10-067-832D-13 (1-102) x US-11-087-099-10885 (1-3475)
Qy   98 GCTGCAATCAGCTTCTTAAGTCGCCCGATGGTGATCATCGGTGTGCATTAAACGNMGACC 39
    ||| :::: ::: :::: :::: :::: :::: :::: ::::
Db   231 AlaGlyValAenLeuIleLeuAsnProAlaIleThrIleAsnLeuSerGlnSer-GlyMe 250
Qy   38 TTTTTCACGACGCTGCTTGCAA 14
    ||||| :||| :||| :||| :||| :||| :||| :|||
Db   250 tMetSerProAspGlyArgCysLys 258

RESULT 13
US-11-087-099-9005
; Sequence 9005, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9005
; LENGTH: 3488
; TYPE: PRT
; ORGANISM: Planktotoxrix agardhii
US-11-087-099-9005

Alignment Scores:
Pred. No.:      17.4      Length:      3488
Score:          49.00     Matches:      11
Percent Similarity: 62.1% Conservative: 7
Best Local Similarity: 37.9% Mismatches: 10
Query Match:      26.1% Indels:      1
DB:               7       Gaps:        0

US-10-067-832D-13 (1-102) x US-11-087-099-9005 (1-3488)
Qy   98 GCTGCAATCAGCTTCTTAAGTCGCCCGATGGTGATCATCGGTGTGCATTAAACGNMGACC 39
    ||| :::: ::: :::: :::: :::: :::: :::: ::::
Db   231 AlaGlyValAenLeuIleLeuAsnProAlaIleThrIleAsnLeuSerGlnSer-GlyMe 250
Qy   38 TTTTTCACGACGCTGCTTGCAA 14
    ||||| :||| :||| :||| :||| :||| :||| :|||
Db   250 tLeuSerProAspGlyArgCysLys 258

RESULT 14
US-10-821-234-1145
; Sequence 1145, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07

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